



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 176413

TO: Rosanne Kosson
Location: REM/3B84/3C70
Art Unit: 1653
Friday, January 13, 2006
Case Serial Number: 10/615515

From: Kristine Hensle
Location: Biotech-Chem Library
REM-1B69
Phone: (571) 272-4161

Kristine. Hensle@uspto.gov

Search Notes

Examiner Kosson,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

Kristine Hensle
Librarian
STIC Biotech/Chem Library
(571)272-4161

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 13, 2006, 11:06:13 ; Search time 21 Seconds
(without alignments)
2464.982 Million cell updates/sec

Title: US-10-615-515-6
Perfect score: 2787
Sequence: 1 MESSVNOQPLNEKQIANSQ.....MCGFDGALDIVIRNFTLDMI 538

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2787	100.0	538	2 A31760	Ro/SS-A complex, 6
2	2269	81.4	538	2 I51560	ribonucleoprotein
3	1011	36.3	643	2 T19225	Ro autoantigen 60K
4	798.5	28.7	531	2 C75418	ribonucleoprotein
5	180.5	6.5	719	2 S55939	telomerase compone
6	130.5	4.7	1937	2 I38055	myosin heavy chain
7	125.5	4.5	1938	1 JX0178	myosin heavy chain
8	122	4.4	439	2 C64401	hypothetical prote
9	119.5	4.3	876	2 A23767	myosin heavy chain
10	119	4.3	1938	2 A53293	skeletal myosin he
11	118.5	4.3	1157	2 T43259	pyruvate:ferredoxi
12	118	4.2	713	2 S70434	zona pellucida gly
13	118	4.2	836	2 T42323	hypothetical prote
14	117.5	4.2	741	2 S39082	myosin heavy chain
15	117.5	4.2	955	2 S2348	myosin heavy chain
16	116.5	4.2	373	2 G75073	hypothetical prote
17	116	4.2	394	2 T45875	hypothetical prote
18	116	4.2	1024	2 B86331	hypothetical prote
19	115.5	4.1	571	2 H82268	prolyl-cRNA synthe
20	115	4.1	615	2 F64572	arginine decarboxy
21	114.5	4.1	1128	2 G86266	hypothetical prote
22	114.5	4.1	1175	2 T46124	hypothetical prote
23	114.5	4.1	1418	2 S64918	hypothetical prote
24	114	4.1	1351	2 B97273	superfamily I DNA
25	113.5	4.1	1496	2 T05634	hypothetical prote
26	113.5	4.1	2025	2 JCS020	tetrapeptide
27	113	4.1	1577	2 T19722	hypothetical prote
28	112.5	4.0	936	2 S39083	myosin heavy chain
29	111.5	4.0	698	2 S52696	myosin heavy chain

30	111.5	4.0	1606	2 T34073	paranemin - chicle
31	111	4.0	1940	2 A29320	myosin heavy chain
32	110.5	4.0	1157	2 T43258	pyruvate:ferredoxi
33	110.5	4.0	2094	2 S33124	tpi protein - huma
34	110	3.9	15281	2 S41309	cyclosporin synthe
35	109.5	3.9	1948	2 S00485	gene 11-1 protein
36	109	3.9	478	2 D30169	leukotoxin secreti
37	108.5	3.9	1179	2 P71190	probable chromosom
38	107.5	3.9	1039	2 S81819	myosin heavy chain
39	107.5	3.9	1085	2 F96712	hypothetical prote
40	107	3.8	533	2 T36919	hypothetical prote
41	106.5	3.8	1940	1 A24922	myosin heavy chain
42	106	3.8	394	2 B89780	ornithine aminotra
43	106	3.8	703	2 T48559	probable receptor-
44	106	3.8	1033	2 A86714	hypothetical prote
45	105.5	3.8	420	2 S55272	DNA-binding protei

ALIGNMENTS

RESULT 1
A31760
Ro/SS-A complex, 60K ribonucleoprotein - human
C:Species: Homo sapiens (man)
C:Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 09-Jul-2004
C:Accession: A31760; A30596
R:Deutscher, S.L.; Harley, J.B.; Keene, J.D.
Proc. Natl. Acad. Sci. U.S.A. 85, 9479-9483, 1988
A:Title: Molecular analysis of the 60-kDa human Ro ribonucleoprotein.
A:Reference number: A31760; MUID:89071722; PMID:3200833
A:Accession: A31760
A:Molecule type: mRNA
A:Residues: 1-538 <DED>
A:Cross-references: UNIPROT:P10155; UNIPARC:UPI00004EEBA; GB:J04137; NID:g177782; PIND:f
R:Ben-Chetrit, E.; Gandy, B.J.; Tan, R.M.; Sullivan, K.F.
J. Clin. Invest. 83, 1284-1292, 1989
A:Title: Isolation and characterization of a cDNA clone encoding the 60-kD component of t
A:Reference number: A30596; MUID:89198084; PMID:2649513
A:Accession: A30596
A:Molecule type: mRNA
A:Residues: 1-238, 'R', 240-292, 'DV', 295-300, 'A', 302-514, 'ALONTLANKSF' <BEN>
A:Cross-references: UNIPARC:UPI0000179866; GB:M25077; NID:g387656
A:Note: the sequence is revised in Genbank entry HUMANTARNP, release 111.0, (PID:g387657)
C:Genetics:
A:Gene: GDB:SSA2
A:Cross-references: GDB:355563; OMIM:600063
A:Map position: 1q31-1q31
C:Keywords: DNA binding; zinc finger
F:305-323/Region: zinc finger CCH motif
Query Match 100.0%; Score 2787; DB 2; Length 538;
Best Local Similarity 100.0%; Pred. No. 1.66-181;
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MESSVNOQPLNEKQIANSQSGYVQVTDNRIHFLFCGSGGYYIKKQGLGEMEA 60
DB 1 MESSVNOQPLNEKQIANSQSDYVQVTDNRIHFLFCGSGGYYIKKQGLGEMEA 60
QY 1 LRLLEDGRCGVIOEIKSFSQEGRTTKOEPMLFALAIQSGSDISTKQAFKAVSEVCR 120
DB 1 LRLLEDGRCGVIOEIKSFSQEGRTTKOEPMLFALAIQSGSDISTKQAFKAVSEVCR 120
QY 121 IFTHLFTFIQPKDDKESNKGCMGRALRKALADWYNEKGNALALAVTKYQRNGWSHK 180
DB 121 IFTHLFTFIQPKDDKESNKGCMGRALRKALADWYNEKGNALALAVTKYQRNGWSHK 180
QY 181 DILRLSHLKPSSGGLAIVTKYITTKGKVEHETKKAHSVETBEKLLKYLEAVEKVRTD 240
DB 181 DILRLSHLKPSSGGLAIVTKYITTKGKVEHETKKAHSVETBEKLLKYLEAVEKVRTD 240
QY 241 ELEVLHLEHRLVBEHLLTNHLKSKVEVKALLQEMPLTALLRNIGKQTANSVLBERGNS 300
DB 241 ELEVLHLEHRLVBEHLLTNHLKSKVEVKALLQEMPLTALLRNIGKQTANSVLBERGNS 300

Db 241 ELEVIHILIEBHRLVREHLTNHLKSKKEVKALLQEMFULTALLRLNLGKMTANSVLEPGNSE 300

QY 301 VSLVCEKLCNEKLLKKARIPHFLILALETYKTHGIRGLKRRPDEIILKALDAAYKT 360

Db 301 VSLVCEKLCNEKLLKKARIPHFLILALETYKTHGIRGLKRRPDEIILKALDAAYKT 360

QY 361 FKTYEPTGKFFLAVDSASNNORVLGSIINASTVAAMCMTVTRTKDSYVAFSDENV 420

Db 361 FKTYEPTGKFFLAVDSASNNORVLGSIINASTVAAMCMTVTRTKDSYVAFSDENV 420

QY 421 PCPVTDMTLOQVLMANSQIPAGGTDCLPMVMAQKNTPADVFIVFTDNETFAGVHPA 480

Db 421 PCPVTDMTLOQVLMANSQIPAGGTDCLPMVMAQKNTPADVFIVFTDNETFAGVHPA 480

QY 481 IALREYRKMDIPAKLIVCGMTSNGFTIADPDDRGMLDMCGFDGALDVIRNFTLDMI 538

Db 481 IALREYRKMDIPAKLIVCGMTSNGFTIADPDDRGMLDMCGFDGALDVIRNFTLDMI 538

RESULT 2

151560 ribonucleoprotein - African clawed frog
C/Species: Xenopus laevis (African clawed frog)
C/Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C/Accession: 151560
R/O'Brien, C.A.; Margelot, K.; Molin, S.L.
Proc. Natl. Acad. Sci. U.S.A. 90, 7250-7254, 1993
A/Title: Xenopus Ro ribonucleoproteins: members of an evolutionarily conserved class of
A/Reference number: A48294; MUID:93348251; PMID:7688474
A/Accession: 151560
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-538 <OXB>
A/References: UNIPROT:P42700; UNIPARC:UPI000013450E; GB:L15430; NID:g295535; PIDD:

Query Match 81.4%; Score 2269; DB 2; Length 538;
Best local Similarity 78.6%; Pred. No. 2,4e-146;
Matches 423; Conservative 59; Mismatches 56; Indels 0; Gaps 0;

QY 1 MEESVNOMQPLNEKQINSODGYVQVTDNMRHLRFLCFSGSGGTYIIEKQGLGENAE 60

Db 1 MEAMMDQTOPLNKQVNSBEGYVQVSDMNRRLRFLCFSGSGGTYIIEKQGLGENAE 60

QY 61 LIRLIEGRGCEVQEIETSPQSEGRRTTKQBPMLFALMISGCSPISTKQAFKAVSVCR 120

Db 61 LIRLIEGRGCEVQEIETSPQSEGRRTTKQBPMLFALMISGCSPISTKQAFKAVSVCR 120

QY 121 IPTHLETFIOFKDOLKESMKCGMWRALRKALADWYNEKGGMALALAVTYKKORNGSHK 180

Db 121 IPTHLETFIOFKDOLKESMKCGMWRALRKALADWYNEKGGMALALAVTYKKORNGSHK 180

QY 181 DLRLSLHKSSBGLAVTKYITGKMKVHELYEKALSVTEKGLKYLEAVENKRYTKD 240

Db 181 DLRLSLHKSSBGLAVTKYITGKMKVHELYEKALSVTEKGLKYLEAVENKRYTKD 240

QY 241 ELLEVIHILIEBHRLVREHLTNHLKSKKEVKALLQEMFULTALLRLNLGKMTANSVLEPGNSE 300

Db 241 ELLEVIHILIEBHRLVREHLTNHLKSKKEVKALLQEMFULTALLRLNLGKMTANSVLEPGNSE 300

QY 301 VSLVCEKLCNEKLLKKARIPHFLILALETYKTHGIRGLKRRPDEIILKALDAAYKT 360

Db 301 VSLVCEKLCNEKLLKKARIPHFLILALETYKTHGIRGLKRRPDEIILKALDAAYKT 360

QY 361 FKTYEPTGKFFLAVDSASNNORVLGSIINASTVAAMCMTVTRTKDSYVAFSDENV 420

Db 361 FKTYEPTGKFFLAVDSASNNORVLGSIINASTVAAMCMTVTRTKDSYVAFSDENV 420

QY 421 PCPVTDMTLOQVLMANSQIPAGGTDCLPMVMAQKNTPADVFIVFTDNETFAGVHPA 480

Db 421 PCPVTDMTLOQVLMANSQIPAGGTDCLPMVMAQKNTPADVFIVFTDNETFAGVHPA 480

QY 481 IALREYRKMDIPAKLIVCGMTSNGFTIADPDDRGMLDMCGFDGALDVIRNFTLDMI 538

Db 481 IALREYRKMDIPAKLIVCGMTSNGFTIADPDDRGMLDMCGFDGALDVIRNFTLDMI 538

Db 481 TALQYREKMGIPAKLIVCGMTSNGFSIADPDDRGMLDICGDSGALDVIRNFTLDMI 538

RESULT 3

T19225 Ro autoantigen 60k homolog - Caenorhabditis elegans
N/Alternate names: Rop1p protein
C/Species: Caenorhabditis elegans
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C/Accession: T19225; J04574; T26556
R/McMurray, A.
Submitted to the EMBL Data Library, June 1996
A/Reference number: Z19092
A/Accession: T19225
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-643 <MIL>
A/Cross-references: UNIPROT:Q27274; UNIPARC:UPI000013450C; EMBL:Z73969; PIDD:CAA98241.1;
A/Experimental source: clone C12D8
R/Labbe, J.C.; Jannatipour, M.; Rokeach, L.A.
Gene 167, 227-231, 1995
A/Title: The Caenorhabditis elegans rop-1 gene encodes the homologue of the human 60-kDa
A/Reference number: J04574; MUID:96144279; PMID:8566782
A/Accession: J04574
A/Molecule type: mRNA
A/Residues: 1-643 <LAB>
A/Cross-references: UNIPARC:UPI000013450C; GB:U21487; NID:g905358; PIDD:AAA96949.1; PID:5
R/Gardner, A.
Submitted to the EMBL Data Library, January 1998
A/Reference number: Z20231
A/Accession: T26556
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-643 <M12>
A/Cross-references: UNIPARC:UPI000013450C; EMBL:AL021479; PIDD:CAA16325.1; GSPDB:GN00023;
A/Experimental source: clone Y22F5A
C/Comment: This protein is a main protein constituent associated with the RNA in the Ro 1
C/Genetics:
A/Gene: rop-1
A/Map position: 5; V
A/Introns: 24/2; 272/3; 329/2; 545/3
F:139-333/Dominant: RNA binding #statue predicted <RNB>
F:140-145/Region: ribonucleoprotein similarity
F:189-197/Region: ribonucleoprotein similarity
F:291-295/Region: nuclear location signal
F:419-422/Region: nuclear location signal
F:588-591/Region: nuclear location signal

Query Match 36.3%; Score 1011; DB 2; Length 643;
Best local Similarity 36.3%; Pred. No. 7.8e-61;
Matches 215; Conservative 111; Mismatches 204; Indels 62; Gaps 9;

QY 7 QMOPLNKQIANSODGYVQVTDNMRHLRFLCFSGSGGTYIIEKQGLGENAEALYLLIE 66

Db 54 QMEKVDQGVENNAAGFVPEVSDETOVRRLILGSDGSHQSEKITTIDNAGRILKIE 113

QY 67 DGRGCEVIOEIKSPQSEGRRTTKQBPMLFALMISGCSPISTKQAFKAVSVCR 120

Db 114 QGNGHMLKALILINENRPPKRNAMFTLALICARLSTHDYTKTTCBPMLNANSDYTRAL 173

QY 110 -AFAFVSEVCRIPHLETFIOFKDOLKESMKCG-----MMGRALRKALADWYNEKG 161

Db 174 HDSALDLIPVCRTPHLETFVYCGTISSTYAGGAKSSTGWSRNRNISKWYTTKT 233

QY 162 MALALAVTYKKORNGSHKDLRLSH--LKPSSGLA-----IVTKYITG----- 205

Db 234 EKLAMLLTKYPRQSEGRSHRDLFRILAHNPLNDSHSGSEDLRLRBOQLFRFAVVGDLVYRK 293

QY 206 -----KQGVHLYEKALSV-----ETKLLKYLEAVENKRYTKDELEVHILI 248

Db 294 RKNVSVEEVAEVEVWDKAKLKYTEEQILKEQSRALNVEVYLLKLNQSESEVIAAI 353

QY 249 EHRVLVREHLTNHLKSKKEVKALLQ-EMFULTALLRLNLGKMTANSVLEPGNSEVSLVCEK 307

```
Db      354  KKGLVSEHLPPTSLSNKLWEHLPDVSMETNARIKLAKTTVVGALD--EKRDNIYKR 411
      308  LCNKELKKARIHHPHILIALETYKTHGKGLKMRPDEBILKALDAFYKTEKVEPT 367
      412  LTQGEELRBSRIHINILTLAAVYAQGRGDKSLTWBPNQKICDALEAGFYKAFVNAPEPT 471
Qy      368  GKRFLLAVDVASAMQRYLGSILNASTVAAAMCVNTRTEKDSYVVAFSDMVCPTTD 427
      472  GKRYCLALDVSGSMTSRVSSEPLSCREAAVTGMSLINLNEAEVRCVAFCDKLTLPFTKD 531
Db      428  MTLQOVLMAHQIAGGTDGSLPMIWAOKTTPADVIFVFTDNETFAGGVAPALAEYR 487
      532  WKIQGVNDVYNNIDFGRTDGLPMTWATENNLLKDFVFIITDNDTWAGEIRPFPAIKYR 591
Qy      488  KROMDI-PAKLIVCGMTSNGFTIADPDDRGMLDMCGFDGTALDVIRNFTLDMI 538
      592  EASGIHAKYIVVMAQAVDYSIADPSDAGMLDITGFDASVQIVHEFVTGKI 643
Db
```

RESULT 4

```
C75418
ribonuclease protein Ro/SS-A-related protein - Deinococcus radiodurans (strain R1)
C:Species: Deinococcus radiodurans
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: C75418
R:White, O.; Bisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamathevan, J.U.; Lam, P.; McDonald, L.; Uetzerback, T.; Zalewski, C.; Ma
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A:Reference number: A75250; MUID:20036896; PMID:10567266
A:Accession: C75418
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-531 <WHI>
A:Cross-references: UNIPROT:Q9RUW8; UNIPARC:UPI000013450D; GB:AE001973; GB:AE000513; NID
A:Experimental source: strain R1
C:Genetics:
A:Gene: DR1262
A:Map position: 1
```

```
Query Match      28.7%; Score 798.5; DB 2; Length 531;
Best Local Similarity 35.7%; Pred. No. 1.6e-46;
Matches 190; Conservative 92; Mismatches 225; Indels 25; Gaps 8;
```

```
Qy      7  QMQLPLKQIANSQGYVQVTDNRILHRLCFGSEGGTYIKKQKLGLENALILRIIE 66
      15  QTERLDERQVRNNAAGFYVTVSDERLTRLVLGVGGTFYASQKHTVQATDFVRELQ 74
Db      67  DORGEVIOEIKSFQSEG-RTTKQEPMLPALAISCOS-DISTKQAFYAVSEVCRIPTH 124
      75  --KDAALALRVTLDVVRGGRAPKADBALVTLALIAKTANADRYAAMWALEVARTGM 132
Qy      125  LFTFIQPKDKESMKCGMRALRAIADWYNEKGAMALAVTKYKORNGMSHKDLIR 184
      133  LHLFLAFADAL-----GGWGRLLTRGVANVETADVDTALMAVYKARDMSQADALR 186
Db      165  LSHLKPSSEGLAVTKYTKGMEVHELKELASVETEKLYLEAVKVKRTQDELEV 244
      187  KAHPTDDAARNAVVKFVWDG-----VLPRVDSPALRVLEGHLKATEAQTDAAA 235
Qy      245  IHLREHRLVREHILTNHLKSKVWVALLQEMPLTALLNLSGMTANSVLEPGNS-EVSL 303
      236  AALMDSYRPLAEVPT-HVRGAEVYRAAMQNTGLTLLNLSGLNGVGLTRPDSATVQA 294
Db      295  VIERLTDPAALKGRHHPDLAKARLVVAQGVGRKGTWLPVPRVVDALIEAFTLAFCN 354
Qy      304  VCEKLCNEKLLKKARIHHPHILIALETYTKGHLGKGLKMRPDEBILKALDAFYKTEPT 363
      364  VERTGRFLAVDVASAMQRYLGSILNASTVAAAMCVNTRTEKDSYVVAFSDMVCPT 421
      355  VOPANTRHLLALDVSGSMTCGVAVGPGLTPNMAAAMSLIALRTPEPALTWGFAEQFRP 414
Db
```

```
Qy      422  CPVTTDMLQOVLMAHQIAGGTDGSLPMIWAOKTTPADVIFVFTDNETFAGGVAPAI 481
      415  LGIRPRTLSANQKQASMSFGTDCAQPIILMAQBLDVDTFVYVYDNETWAGVHPTV 474
Db      482  ALREYRKMDIPAKLIVCGMTSNGFTIADPDDRGMLDMCGFDGTALDAVIRNF 533
      475  ALDQYQKMGAPRLIVVGLTATEFSSIADPQRRLMDLVGFDAAAPVMTAF 526
Db
```

RESULT 5

```
S55939
telomerase component p80 - Tetrahymena thermophila
C:Species: Tetrahymena thermophila
C:Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C:Accession: S55939
R:Collins, K.; Kobayashi, R.; Greider, C.W.
Cell 81, 677-686, 1995
A:Title: Purification of Tetrahymena telomerase and cloning of genes encoding the two pr
A:Reference number: S55939; MUID:95292335; PMID:7774009
A:Accession: S55939
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-719 <COL>
A:Cross-references: UNIPROT:Q94818; UNIPARC:UPI0000136878; EMBL:U25641; NID:g862483; PID
A:Genetic code: SGC5
```

```
Query Match      6.5%; Score 180.5; DB 2; Length 719;
Best Local Similarity 20.7%; Pred. No. 0.00022;
Matches 115; Conservative 100; Mismatches 191; Indels 149; Gaps 29;
```

```
Qy      102  CSDISTKQAAKAVSEVCRITHTLFTFIQPKDKESMKCGMWGRALRAIADWYNEKG 161
      193  CTESQKKTKMFRYLS-----VTNQKMDQTKKKRKENLTLTL--QATSEBDSKSRRTGD 245
Db      162  M-----ALAAVTK--YKORNGMSHKDLIRLSHLK-PSSEGLAIVTKYTKGMEVH 210
      246  IHWVEDAIKALKPRAVKKIARQAMK-----KHMARPKIPNLTLSKYLIT-----FK 293
Qy      211  ELYKEKALSVETEKLLKYLEAVEKVKRTQDELEVH-----LIEHRLVREHILIT 260
      294  DLKFCCHISBPERERYKILG--KKYKTEBEYKAFGDSASAFNPRLAGKMKIEISKT 351
Db      261  --NHLKSR---EYWKALL--QEMPLTALLNLSGMTANSVLEPGNSEV--SLVEKLCN 310
      352  WENELSAKGNTAFVMDNLISSNQLPYMAMLRNL-----SNILKAGVSDTTHSIVINKIC 406
Qy      311  EKLKKARIHHPHILIALETY-----KTGHGARGKL-----KWRPDE 347
      407  PRAVENSKMPFLQFSALEAVNEAVTKGPKAKKRENNMLKQIIEAVKVEKTEDEKKDM 466
Db      348  EILKALDAAFYKTFKVEPTGRFL-----LAV-----DVSASMNOR 384
      467  ELHQTBEGER---VAVNGSIGQYINSLTELAKIVNNKULDEIKGHTAIFSDVSGSMSTS 523
Qy      385  VLGSIINASTVAAAN-----CQVVTTEKDSYVV--AFSDMVCPTTDM----- 428
      524  MSGAKKYGSVATCECALVLGLAMVORCEKSSFYIFSPSSQCKCYLEVLDLPGDELPR 583
Db      429  TLQOVLMAHQIAGGTDGSLPMI--WAOKTTPADVIFVFTDNETFAG-----GVAP 479
      584  SMQKLOEKRGKL--GGGTDPPEYCIDEMT--KNTKHYDNVILSDMMIABGYSIDINRGSSI 641
Qy      480  AIALREYRKMDIPAKLIVCGMTSNG--FTIADP--DDRGMMLDMCGFDGTAL----- 527
      642  VNSIKKYKDVAVPNKIFAVVDLEGGKCLNLDBEFENNYYIKIFGMSDSLKFIASKQGG 701
Db      528  ---DVIRNFTLDMI 538
      702  ANNVEYIKNPAFOKI 716
Db
```

RESULT 6

138055 myosin heavy chain, perinatal skeletal muscle - human

N/Contains: myosin ATPase (EC 3.6.4.1)

C/Species: Homo sapiens (man)

C/Date: 17-May-1996 #sequence revision 17-May-1996 #text change 09-Jul-2004

C/Accession: 138055; JH0154; S12459; S09332; A30220; S49478

R/Jullian, E.H.; Kelly, A.M.; Pomidov, A.J.; Hoffman, R.; Schiaffino, S.; Steadman, H.H.; Eut. J. Biochem. 230, 1001-1006, 1995

A/Title: Characterization of a human perinatal myosin heavy-chain transcript.

A/Reference number: 138055; MUID:95324556; PMID:7601129

A/Accession: 138055

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-1937 <RES>

A/Cross-references: UNIPROT:P13535; UNIPARC:UPI000016ADAD9; EMBL:Z38133; NID:9558668; PIR:Karsch-Mizrachi, I.; Feghali, R.; Shows, T.B.; Leinwand, L.A.

Gene 89, 289-294, 1990

A/Title: Generation of a full-length human perinatal myosin heavy-chain-encoding cDNA.

A/Reference number: JH0154; MUID:90323631; PMID:2373371

A/Accession: JH0154

A/Molecule type: mRNA

A/Residues: 1-14, 'A', 16-859 <KAR>

A/Cross-references: UNIPARC:UPI000017760F; GB:Y00821

A/Experimental source: skeletal muscle

R/Bober, E.

Submitted to the EMBL Data Library, January 1989

A/Reference number: S12458

A/Accession: S12458

A/Molecule type: mRNA

A/Residues: 502-1071, 'N', 1073-1250, 'DGG', 1253-1376, 'NT', 1379-1913, 'D', 1915-1937 <BOB>

A/Cross-references: UNIPARC:UPI000016A5F8; EMBL:X51592; NID:929465; PIRN:CA35941.1; PIR:Bober, E.; Buchberger-Seidl, A.; Braun, T.; Singh, S.; Goedde, H.W.; Arnold, H.H.

Eur. J. Biochem. 189, 55-65, 1990

A/Title: Identification of three developmentally controlled isoforms of human myosin heavy chain

A/Reference number: S09331; MUID:90235862; PMID:1691980

A/Accession: S09332

A/Molecule type: mRNA

A/Residues: 502-547, 'X', 549-617, 'X', 619-687, 'X', 689-757, 'X', 759-827, 'X', 829-897, 'X', 899-1376, 'NT', 1379-1386, 'X', 1388-1456, 'X', 1458-1526, 'X', 1528-1596, 'X', 1598-1666, 'X', 1668-17

A/Cross-references: UNIPARC:UPI0000177610; EMBL:X51592

R/Feghali, R.; Leinwand, L.A.

J. Cell Biol. 108, 1791-1797, 1989

A/Title: Molecular genetic characterization of a developmentally regulated human perinatal myosin heavy chain

A/Reference number: A30220; MUID:89234168; PMID:2715179

A/Accession: A30220

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 860-969, 'Q', 971-1246, 'H', 1248-1260, 'G', 1262-1296, 'Q', 1298-1503, 'AH', 1506-184

A/Cross-references: UNIPARC:UPI0000177611; GB:Y00821; NID:934863; PIRN:CA68757.1; PIR:G

C/Genetics:

A/Gene: GDB:MYH8

A/Cross-references: GDB:125267; OMIM:160741

A/Map position: 17pter-17p12

C/Superfamily: myosin heavy chain; myosin motor domain homology

C/Keywords: actin binding; ATP; coiled coil; hyaluronase; muscle contraction; nucleotide b

F/91-769/Domain: myosin motor domain homology <MOTOR>

F/181-188/Region: nucleotide-binding motif A (P-loop)

F/551-588/Region: actin binding #status predicted

F/658-680/Region: actin binding #status predicted

F/842-1282/Region: S2 #status predicted

F/938, 708/Active site: Cys #status predicted

Query Match 4.7%; Score 130.5; DB 2; Length 1937;

Best Local Similarity 20.0%; Pred. NO. 2.1;

Matches 101; Conservative 72; Mismatches 168; Indels 165; Gaps 18;

QY 1 MEESVNMQNPINERQ-----IANSQGYWQVTDMRRLHRLFCGSGGTY 47

DB 1255 LEDVSEIKTEKEEQRLINDLQARALQTEAGYRSQLEKDALVSQLSRSKQASTQ 1314

QY 48 IKKQKLGLEN-----AALIRLIEDGR-GCEVIQETIKSRSGSGRTTKQEPMLFALAIQSC 102

DB 1315 IEEELKQLEHEETKAKVALAHALQSSRHDCDLLEQYEEBEGKAEILQ----- 1361

QY 103 SDISTKQAPKAVSEVCRIPTHLFT-FIQCKDLKE-----SMKCG 142

DB 1362 -----RLSKANSEVAQWTKYETDALIQTEELERKKKLAQRLQAEHVEAVNAKCA 1415

QY 143 MMGRALRKAIADWYNEKGWAL-----ALATYKKQRN-----GMSHK----- 180

DB 1416 -----SLKTKQRQNEVEDLMDVERSNMAACALDKQRNFDKVLSEMKQKVESTQALE 1471

QY 181 -----DLRLSHL-----KPSSEGLAVTKYTKGKVEHLYK 214

DB 1472 ASQKESRLSTELFKVKNVVEESLDQLETLRRKNKLQCEISDLTEQIAGSGQIHLEK 1531

QY 215 EKSLSTETELKYLKLAVERKRTKDELEVINHLEHRVLRHLLTNHLSKVEWKLQ 274

DB 1532 IKK-QVEQKRC-----EIQALAEAEASLEHEGKILRIQLELNQVRSVDRTAK 1582

QY 275 EMPFLTLRLGLGM--TANSLBPG-----NSEVSLVCEK 307

DB 1583 DEEIDQLKRNHTVETWQSTLDABTRSDALRYKKMGEGDLENMELQNHANRLAAS 1642

QY 308 LCN-----EKLKKARLHPHILLALETYKTGHLRGKLRKRPDEILK---ALDAAFYK 359

DB 1643 LRNVYNTQGIKETEQLH-----LDLALRGQEDLEKQLAIVERBANLLQAEIEE 1690

QY 360 TFKTVPTGRFLIANDVSAAMQRY 385

DB 1691 LWTATLEOTERSRKIRARQELLDASERV 1716

RESULT 7

JX0178 myosin heavy chain, fast skeletal muscle, adult [validated] - chicken

N/Contains: myosin ATPase (EC 3.6.4.1)

C/Species: Gallus gallus (chicken)

C/Date: 31-Dec-1993 #sequence revision 31-Dec-1993 #text change 31-Dec-2004

C/Accession: PX0050; PX0051; PX0052; JX0178; A26365; S02082; PM0009; S39081; S24351; S055

R/Hayashida, M.; Maeda, T.; Matsuda, G.

J. Biochem. 110, 54-59, 1991

A/Title: The primary structure of skeletal muscle myosin heavy chain: I. Sequence of the

A/Reference number: PX0050; MUID:92041767; PMID:1939027

A/Accession: PX0050

A/Molecule type: protein

A/Residues: 1-205 <HAY>

A/Cross-references: UNIPROT:Q90913; UNIPROT:Q90909; UNIPARC:UPI0000173E18

R/Komine, Y.; Maeda, T.; Matsuda, G.

J. Biochem. 110, 60-67, 1991

A/Title: The primary structure of skeletal muscle myosin heavy chain: II. Sequence of the

A/Reference number: PX0051; MUID:92041768; PMID:1939028

A/Accession: PX0051

A/Molecule type: protein

A/Residues: 206-636 <KOM>

A/Cross-references: UNIPARC:UPI0000173E19

R/Maeda, T.; Miyanihira, T.; Matsuzono, K.; Tanloka, Y.; Matsuda, G.

J. Biochem. 110, 68-74, 1991

A/Title: The primary structure of skeletal muscle myosin heavy chain: III. Sequence of the

A/Reference number: PX0052; MUID:92041769; PMID:1939029

A/Accession: PX0052

A/Molecule type: protein

A/Residues: 201-213, 632-837 <MAI>

A/Cross-references: UNIPARC:UPI0000173E1A; UNIPARC:UPI0000173E1B

R/Maeda, T.; Yajima, E.; Negata, S.; Miyanihira, T.; Nakayama, S.; Matsuda, G.

J. Biochem. 110, 75-87, 1991

A/Title: The primary structure of skeletal muscle myosin heavy chain: IV. Sequence of the

A/Reference number: JX0178; MUID:92041770; PMID:1939030

A/Accession: JX0178

A/Molecule type: protein

A/Residues: 833-1938 <MA2>

A/Cross-references: UNIPARC:UPI0000173E1C

R/Maeda, T.; Hayashida, M.; Tanloka, Y.; Komine, Y.; Matsuda, G.

Proc. Natl. Acad. Sci. U.S.A. 84, 416-420, 1987

A: Molecule type: DNA
 A: Residues: 1-836 <ALO>
 A: Cross-references: UNIPROT: O4483; UNIPARC: UP1000009B4F3; EMBL: X97918; P1DN: CAA66530.1
 C: Superfamily: phage SPPI hypothetical protein 32

Query Match 4.2%; Score 118; DB 2; Length 836;
 Best local similarity 19.0%; Pred. No. 4.7;
 Matches 96; Conservative 82; Mismatches 159; Indels 168; Gaps 23;

128 P10FKK-----DLKSNKCGMGDALKKAIADWN-----EKGGMALAL 166
 36 FFOYKKNIEYTVRIIPHADVTNNKK-RLM-----KAIHKMYELDSDPSRIEKGGMFT- 88
 167 AVTKYKQKRNKSHDLRLSHLKSSSGLAIVTKYTKMKVEVHELYKERALSTETKLL 226
 89 -----YRKDYFWVDILFRMKNKRSVEFYVSTYK-----QADKTK 125

227 KYLEAVEKVKRTKDELVEVHL-----IEHRLVREHLLTNHLKSEVKALLQEMPL 278
 126 KKEE--NKVARTTEASVKEIAVPLENTILOEMRYLGHDIPTLTNSNDV-----KTP1 177
 279 TALLRNKGRKTVANSVLEPGNSEVSLVCEKLCNEKLLKKARIHPHILLALETYTGHLR 338
 178 SNLL-----NVVDLQDDGDFARFVSCSESRQKWKVNAH--WAYEKVK-----R 221
 339 GKLKMRD-----BEILKALDAAPYKTKVEP---TGKR 370
 222 GKVPQRDALTAKKLTJTGKRVIAAGCINEVNSLSDALQALSNSEFKTEKTKMKKVIKG 281
 371 FLAVDVASAMNQGVLSI-----LNASTVAAMCMVVTREKDSYVA 414
 282 HALDEIGATRFSEHKENLPVFKSRIVAAHAKNRILRDTMAESLALSTLDLSF----- 335
 415 FSDMEVPCVPTDNTLQVILMAISQIPAGTCSLPMIWAQKTVTPADVPIVFTDN-ETF 473
 336 -SNELQGVKVFPRKRREIILNEMNTLSV-----SARTKTDGVNVLSTDEMNKL 383
 474 AGCHNPALALREY-----RKMDTPAKL-----IYCGTS-NG-----FTIADPD 513
 384 AMMPKPDLRKIVADTSLVKKQVEVEIPAVNRDESGIYLGSSEIKGEKIPVMPVTPND 443
 514 --RGMLDMCGFPTGALDVIRNFTLD 536
 444 FYRGYTFIIGGAGAGKDTAIKMWVD 468

RESULT 14
 S39082
 myosin heavy chain, embryonic - chicken (fragment)
 C: Species: Gallus gallus (chicken)
 C: Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 31-Dec-2004
 C: Accession: S39082; S24349; A30170; S01265
 R: Moore, L.A.; Arizubietta, M.J.; Tidjman, W.E.; Herman, L.A.; Bandman, E.
 J. Mol. Biol. 225, 1143-1151, 1992
 A: Title: Analysis of the chicken fast myosin heavy chain family. Localization of isoform submitted to the EMBL Data Library, August 1991
 A: Description: Analysis of the chicken fast myosin heavy chain family: Localization of isoform
 A: Reference number: S39081
 A: Accession: S39082
 A: Status: nucleic acid sequence not shown
 A: Molecule type: mRNA
 A: Residues: 1-741 <MOO>
 A: Cross-references: UNIPROT: O91983; UNIPARC: UP100001775F3; EMBL: M74086
 A: Experimental source: clone Cemb3
 R: Moore, L.A.; Arizubietta, M.J.; Tidjman, W.E.; Herman, L.A.; Bandman, E.
 J. Mol. Biol. 225, 1143-1151, 1992
 A: Title: Analysis of the chicken fast myosin heavy chain family. Localization of isoform
 A: Reference number: S24348; MUID: 92309413; PMID: 1377278
 A: Accession: S24349
 A: Molecule type: mRNA
 A: Residues: 1-12,14-741 <MOO2>
 A: Cross-references: UNIPARC: UP100001775F4; EMBL: M74086
 A: Experimental source: clone Cemb3
 R: Lagrutta, A.A.; McCarthy, J.G.; Scherzinger, C.A.; Heywood, S.M.
 DNA 8, 39-50, 1989
 A: Title: Identification and developmental expression of a novel embryonic myosin heavy-

A: Reference number: A30170; MUID: 89210285; PMID: 2707122
 A: Accession: A30170
 A: Molecule type: DNA
 A: Residues: 723-741 <LAG>
 A: Cross-references: UNIPARC: UP100000FD7DB; GB: M24691; NID: g341219; P1DN: AAA48950.1; PID: 6
 A: Nucleic Acids Res. 15, 8069-8085, 1987
 A: Title: A long polyuridine/polypurine tract induces an altered DNA conformation on ct
 A: Reference number: S01265; MUID: 88040428; PMID: 3671071
 A: Accession: S01265
 A: Molecule type: DNA
 A: Residues: 723-741 <MCC>
 A: Cross-references: UNIPARC: UP100000FD7DB; EMBL: X06251; NID: 963600; P1DN: CAA29593.1; PID:
 C: Superfamily: myosin motor domain homology
 C: Keywords: actin binding; ATP; coiled coil; muscle

Query Match 4.2%; Score 117.5; DB 2; Length 741;
 Best local similarity 20.9%; Pred. No. 4.3;
 Matches 75; Conservative 51; Mismatches 125; Indels 107; Gaps 13;

2 EESVNOQPLNEK--QIANSQDYVWQYDMNLRHFLCGSGGTYYIEKQVLGEN-- 57
 69 EEHQRMINDNTGRARLQTEAGEYSRQVERKDALISQSRGQAFYQIELKRLHEEI 128
 58 --AEALIRLIEDGR-GCEVIOEIKSFQSGRTTKQEPMLPALAICSQCSDISTKQAFKA 114
 129 KAKGALLAHALQSRHDCDLREGEYEEQKGLQ-----RALSKA 169
 115 VSEVCRIPTHLFT-FIQPKDLKSNK----- 140
 170 NSEVAGWRTKCTEDALQRTLEELKAKKLAQLQDAEHEVAVNAKCASTKTKQRLONE 229
 141 -----CGMGKALR---KAIADW---YNEKG-----MALALAVTKKQ 173
 230 VEDLMIDVERANAAACALDKQKNPDKITLAEWQKKEETOAELEBASQKERSJSTELFKM 289
 174 RINGSHKDLRLSL-----RPSSEGLAIVTKYTKMKVEVHELYKERALSVETKTL 226
 290 KNAVEES---LDHLQTLKRNKNLQGEISDLTEQLAEGKAIHELEKVKK-QIEGKK-- 342
 227 KYLEAVEKVKRTKDELVEVHLIEHRLVREHLLTNHLKSEVKALLQEMPTALLRN 284
 343 -----SEIQALAEFAEASLEHEGKILRLQLELNQVKSIEDKIAKDEIDQLKEN 394

RESULT 15
 S24348
 myosin heavy chain, embryonic and adult skeletal muscle (clone Cemb2) - chicken (fragment)
 C: Species: Gallus gallus (chicken)
 C: Date: 03-Feb-1994 #sequence_revision 06-Sep-1996 #text_change 31-Dec-2004
 C: Accession: S24348
 R: Moore, L.A.; Arizubietta, M.J.; Tidjman, W.E.; Herman, L.A.; Bandman, E.
 J. Mol. Biol. 225, 1143-1151, 1992
 A: Title: Analysis of the chicken fast myosin heavy chain family. Localization of isoform
 A: Reference number: S24348; MUID: 92309413; PMID: 1377278
 A: Accession: S24348
 A: Status: nucleic acid sequence not shown
 A: Molecule type: mRNA
 A: Residues: 1-955 <MOO>
 A: Cross-references: UNIPROT: O9DGM5; UNIPARC: UP10000177606; EMBL: M74085
 A: Superfamily: myosin motor domain homology
 C: Keywords: ATP; coiled coil; muscle contraction; skeletal muscle; thick filament

Query Match 4.2%; Score 117.5; DB 2; Length 955;
 Best local similarity 19.6%; Pred. No. 6.1;
 Matches 103; Conservative 80; Mismatches 196; Indels 147; Gaps 20;

23 YWQYDMNLRHFLCGSGGTYYIEKQVLGEN---AEALIRLIEDGR-GCEVIOE1 77
 306 YSRQVERKDALISQSRGQAFYQIELKRLHEEIKAKOALAHALQSRHDCDLRBO 365
 78 KSFSQEGRTTKQEPMLPALAICSQCSDISTKQAFKAVSEVCRIPTHLFT-FIQPKDLK 136

```

Db      366 YEEEOEAKGEIQ-----RALSKANSEVAQWRTKCTETAIOITEELE 406
Qy      137 ESMK-----CGMMGRALR 149
Db      407 EAKKKGLQRLQDABEHVEAVAKCASLEKTKQRLQNEVEDIMIVERANAACARLDKKOK 466
Qy      150 ---KAIADW---YNEKGG-----MALALAVTKKQKNGSHKDLRLSHL-----K 189
Db      467 NFDKILAEWKQKYEETQALEASQKESRSLSSTELFKMKNAYEES---LDHLETLKRENK 522
Qy      190 PSSEGLAIVTKYITKGWKEVHELKYEKALSVETEKLLKYLEAVEKVKRTKDELFEVILHLE 249
Db      523 NLQOEISDLTEQIAEGGKAIHELEKVKK-QIEQEK-----SEIQALEEAEASLEHE 573
Qy      250 EHLVREHLITNHLKSKEVWRFALLQEMPLTALRLNLRGM-----TANSVLEPGNSEVSL 303
Db      574 EGKILRLQLELNQVSEIDRKIAEKDEBIDQKRNHLRIVESQSTLDABIRSRREALRL 633
Qy      304 VCEKLCNEKLLKARIRHPFI-LIALETTYKTHGLRGKJK-----WRPDEI----- 349
Db      634 ---KKWEGDINEMEIQLNHANRVAAEAQXNLRNTQGVLRKDTQIHLDDALRTQBDLKEQV 690
Qy      350 -----LKALDAAPYKTFKTEVPTGKRPLAVDVASMNORVLSIINASTVAAMCMNV 403
Db      691 AMVERRANLQAEIETBELPALEQTERSRKVAQEIMDASERV--QLLHTQNTS---LIN 744
Qy      404 TRTEKDSYVVAFSDMVPCTVTDWTLQOVLMAWSQIPAGGTCSL 449
Db      745 TKKULFTDIAQIQSEM-----EDTIQBARNAEBEAKKAITDAAM 783

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Search completed: January 13, 2006, 11:11:13
 Job time : 24 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using bw model

Run on: January 13, 2006, 11:05:17 ; Search time 79 Seconds
(without alignments)
2992.225 Million cell updates/sec

Title: US-10-615-515-6

Perfect score: 2787
Sequence: 1 MEEVNMQNPINERQIANSO.....MCGPDGALDVIRNFTLDMT 538

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_GeneSeq_21.*
1: geneSeqp19806:*
2: geneSeqp19908:*
3: geneSeqp20008:*
4: geneSeqp20018:*
5: geneSeqp20028:*
6: geneSeqp20038:*
7: geneSeqp20038:*
8: geneSeqp20048:*
9: geneSeqp20058:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	2787	100.0	538	5 ABG32657	Abg32657 Human adh
2	2787	100.0	538	8 ADP9190	Adp9190 Sjogren s
3	2787	100.0	552	4 AAB46827	Aab46827 Human ant
4	2782	99.8	553	4 AAB46829	Aab46829 Human ant
5	2782	99.8	553	4 AAB46828	Aab46828 Human ant
6	2659	95.4	525	8 ADP41766	Adp41766 Protein s
7	2659	95.4	525	8 ADS14359	Ads14359 Human SS-
8	1778	63.8	413	2 AAW03717	Aaw03717 Human aut
9	1768	63.4	557	4 AAB94864	Aab94864 Human pro
10	367	13.2	70	2 AAY22511	Aay22511 Human RoR
11	185.5	6.7	641	4 ABB59719	Abb59719 Drosophila
12	180.5	6.5	719	2 AAR96038	Aar96038 80 kD pro
13	143.5	5.1	712	8 ADP6766	Adp6766 Novel hum
14	143.5	5.1	1094	8 ADC30964	Adc30964 Human nov
15	130.5	4.7	1937	8 ADP17289	Adp17289 Human sof
16	130.5	4.7	1937	8 ADP17242	Adp17242 Human sof
17	130.5	4.4	3616	8 ADP45530	Adp45530 Chicken A
18	130.5	4.3	824	7 ADM05888	Adm05888 Human pro
19	130.5	4.3	892	7 ADP79862	Adp79862 Rat myosi
20	130.5	4.3	892	7 ADP47859	Adp47859 Rat Prote
21	130.5	4.3	892	7 ADP47855	Adp47855 Rat Prote
22	119.5	4.3	876	8 ADP17244	Adp17244 Human sof
23	118	4.2	876	2 AAR5194	Aar5194 Porcine z
24	118	4.2	713	2 AAW81804	Aaw81804 Porcine z

25	118	4.2	713	2 AAY42467	Aay42467 Porcine z
26	118	4.2	713	3 AAY52971	Aay52971 Porcine z
27	118	4.2	713	3 AAY82202	Aay82202 Porcine z
28	118	4.2	713	3 AAY52676	Aay52676 Porcine o
29	118	4.2	713	3 AAY52167	Aay52167 Porcine z
30	117	4.2	23	2 AAR43447	Aar43447 Ro/SSA ep
31	116	4.2	22	2 AAR43461	Aar43461 Ro/SSA ep
32	115.5	4.1	550	7 ADB65341	Adb65341 Human pro
33	115.5	4.1	571	6 ABA49243	Ab49243 Protein e
34	115.5	4.1	853	5 ABB93794	Abb93794 Protein e
35	115.5	4.1	1104	8 ADR18225	Adr18225 Mouse GOB
36	115	4.1	561	2 AAW98552	Aaw98552 H. pylori
37	115	4.1	1941	8 ABR53853	Ab53853 Protein s
38	114.5	4.1	1418	6 ABR53853	Ab53853 Protein s
39	114.5	4.1	1418	7 ADK64930	Adk64930 Disease t
40	114.5	4.1	1418	8 ADS43885	Ads43885 Bacterial
41	113.5	4.1	1715	5 AAC22600	Aac22600 Tetraartic
42	113.5	4.1	1715	8 ADS34529	Ads34529 POSH prot
43	113.5	4.1	1792	8 ADS34530	Ads34530 POSH prot
44	113.5	4.1	2000	8 ADN04337	Adn04337 Antipsori
45	113.5	4.1	2000	8 ADP24116	Adp24116 PRO polyp

ALIGNMENTS

RESULT 1
ABG32657
ID ABG32657 standard; protein; 538 AA.

XX AC ABG32657;

DT 15-NOV-2002 (first entry)

XX DB Human adhesion molecule, termed p10155 (Ro60 or ADS5), protein.

XX KW Human; adhesion molecule; ADS1; ADS2; AAC74854.1; Ro60; AAC76768.1;
XX KW p10155; embryogenesis; apoptosis; homeostasis; phenotypic; ligand;
XX KW diagnosis; vaccine; therapeutic; transgenic; knockout; atherosclerosis;
XX KW ischaemia; resection; reperfusion injury; sepsis;
XX KW haematological disease; leukaemia; blood clotting; thrombosis; cancer;
XX KW tumour; metastasis; inflammatory disease; rhinitis;
XX KW gastrointestinal disease; inflammatory bowel disease; ulcerative colitis;
XX KW Crohn's disease; respiratory disease; asthma; COPD;
XX KW chronic obstructive pulmonary disease; respiratory distress syndrome;
XX KW pulmonary fibrosis; immune disorder; autoimmune disease;
XX KW rheumatoid arthritis; transplant rejection; allergy; liver disease;
XX KW cirrhosis; endocrine disease; diabetes; bone disease; osteoporosis;
XX KW neurological disease; stroke; multiple sclerosis; spinal cord injury;
XX KW burn; wound healing; infection; cell-cell adhesion; gene therapy.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Region 373..503 /note= "AD55 adhesion molecule region"

FT Region /note= "Forms the metal ion-dependent adhesion site

FT Region /note= "Forms the metal ion-dependent adhesion site

FT Region /note= "Forms the metal ion-dependent adhesion site

FT Region /note= "Forms the metal ion-dependent adhesion site

FT Region /note= "Forms the metal ion-dependent adhesion site

FT Region /note= "Forms the metal ion-dependent adhesion site

FT Region /note= "Forms the metal ion-dependent adhesion site

FT Region /note= "Forms the metal ion-dependent adhesion site

FT Region /note= "Forms the metal ion-dependent adhesion site

/note= "Forms the metal ion-dependent adhesion site (MIDAS) with residues 376, 378, 380 and 440. Also represents a metal ion ligand along with residues 378 and 380"

WO200262845-A2.

15-AUG-2002.

11-JAN-2002, 2002WO-GB000107.

11-JAN-2001; 2001GB-00000750.

(INPH-) INPHARMATICA LTD.

Gutteridge A, Pagan RJ, Phelps CB;

WPI: 2002-636584/68.

N-PSDB; ABS52589.

New polypeptides comprising adhesion molecules (NCBI Genebank AAC74854.1, AAC76768.1 and P10155), useful for treating, preventing or diagnosing inflammation (e.g. rhinitis), cancers or neurological diseases (e.g. stroke).

Claim 1; Fig 23; 125pp; English.

The invention discloses human adhesion molecule polypeptides (designated ADS1, ADS2 and ADS5 which have the NCBI Genebank accession numbers, AAC74854.1, AAC76768.1 and P10155, respectively.

Adhesion molecules are involved in a wide range of biological processes from embryogenesis to apoptosis. They are essential to the structural integrity and homeostatic functioning of most tissues and, therefore, defects can play a role in many disease processes. Alteration of their activity is a means to alter the disease phenotype. The polynucleotides and polypeptides can be used to identify ligands that bind specifically to, and which preferably inhibit, the adhesion molecule activity, to identify compounds that either increase or decrease the level of expression or activity, for diagnosing a disease in a patient, in a pharmaceutical composition, as a vaccine, for monitoring the therapeutic treatment of disease in a patient, for creating transgenic or knockout animals, expressing higher, lower or absent levels of the ADS polypeptide and for screening a compound effective for treating a disease. The ADS polypeptides, nucleic acids, vectors, ligands, compounds or pharmaceutical compositions, are useful for treating or diagnosing diseases including atherosclerosis, ischaemia, restenosis, reperfusion injury, sepsis, haematological diseases (e.g. leukaemia), blood clotting disorders (e.g. thrombosis), cancer (e.g. lung, prostate, breast, colorectal or brain tumours), metastasis, inflammatory diseases (e.g. rhinitis), gastrointestinal diseases (e.g. inflammatory bowel disease, ulcerative colitis or Crohn's disease), respiratory diseases (e.g. asthma, chronic obstructive pulmonary disease (COPD), respiratory distress syndrome or pulmonary fibrosis), immune disorders (e.g. autoimmune diseases, rheumatoid arthritis, transplant rejection or allergy), liver diseases (e.g. cirrhosis), endocrine diseases (e.g. diabetes), bone diseases (e.g. osteoporosis), neurological diseases (e.g. stroke or multiple sclerosis), spinal cord injury, burns and wound healing or infections (e.g. bacterial infections, particularly *Escherichia coli* infection). The ADS polypeptide is particularly useful as an adhesion molecule or for effecting cell-cell adhesion. The protein sequence presented is the human adhesion molecule, termed P10155 (Ro60 or ADS5)

Sequence 538 AA;

Query Match 100.0%; Score 2787; DB 5; Length 538;

Best Local Similarity 100.0%; Pred. No. 4,2e-244;

Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MEESVNOQPIANEKQIANSOGYVQVTDNRRLRFLFCGSGGGTYTYKEQKLGNNAA 60
 1 MEESVNOQPIANEKQIANSOGYVQVTDNRRLRFLFCGSGGGTYTYKEQKLGNNAA 60

61 LIRLIEDGRGCEVIOEIKSFSGEGRTTKQEPMLFALICSGQSDISTKQAAFKAVSEVCR 120
 61 LIRLIEDGRGCEVIOEIKSFSGEGRTTKQEPMLFALICSGQSDISTKQAAFKAVSEVCR 120

121 IPTHLFFTFIOFKDOLKESMKCGMGRALRKALADWYNEKGMALALAVTKQKNGSHK 180
 121 IPTHLFFTFIOFKDOLKESMKCGMGRALRKALADWYNEKGMALALAVTKQKNGSHK 180

181 DLRLSHLKSPSGIALVTKYITKGWKEVHELYEKALSVETBEKLYLEAVEVYKRTKD 240
 181 DLRLSHLKSPSGIALVTKYITKGWKEVHELYEKALSVETBEKLYLEAVEVYKRTKD 240

241 ELEVIHLIEHRILVREHLTNHLKSKEVYALLQEMPLTALLRNLGHTANSVLEPNSG 300
 241 ELEVIHLIEHRILVREHLTNHLKSKEVYALLQEMPLTALLRNLGHTANSVLEPNSG 300

301 VSLVCEKLCNEKLIKARIRHPHILLALETYKTGHGRLKRRPDEILKALDAARYKT 360
 301 VSLVCEKLCNEKLIKARIRHPHILLALETYKTGHGRLKRRPDEILKALDAARYKT 360

361 FKTYEPTGRKFLAVDVASAMNORVLSIINASTVAAACGVVTRTKDSYVAFSPDEMV 420
 361 FKTYEPTGRKFLAVDVASAMNORVLSIINASTVAAACGVVTRTKDSYVAFSPDEMV 420

421 PCPVTIDMTLQOVLMAMSQIPAGTDCSLPMIWAQKTNTPADVEIVETNETFAGVHPA 480
 421 PCPVTIDMTLQOVLMAMSQIPAGTDCSLPMIWAQKTNTPADVEIVETNETFAGVHPA 480

481 IALREYRKMDIPAKLIVCGMTSNGFTIADPDDRGMLDMCGFDTGALDIVIRNFTLDM 538
 481 IALREYRKMDIPAKLIVCGMTSNGFTIADPDDRGMLDMCGFDTGALDIVIRNFTLDM 538

RESULT 2
 ADR99190 standard; protein; 538 AA.
 ADR99190;
 02-DEC-2004 (first entry)
 Sjogren syndrome antigen A2, SSA2.
 Cytostratic; breast cancer; cancer; human; Sjogren syndrome antigen A2;
 ribonucleoprotein autoantigen SS-A/Ro; SSA2.
 Homo sapiens.
 WO2004078035-A2.
 16-SEP-2004.
 27-FEB-2004; 2004WO-US007268.
 28-FEB-2003; 2003US-0450655P.
 (FARB) BAYER PHARM CORP.
 Eveleigh D, Bigwood D;
 WPI: 2004-653556/63.
 N-PSDB; ADR99063.
 Diagnosing breast cancer comprises comparing the level of expression of PT genes or gene products in a first biological sample taken from a patient with that in a normal patient sample.
 Claim 3; SEQ ID NO 196; 53pp; English.

The present invention relates to a method (M1) for diagnosing breast cancer in a patient. The method comprises comparing the level of expression of one or more genes or gene products in a biological sample from the patient with that in a normal patient sample, where a difference

in the gene expression in the first sample compared to that in the second sample is a diagnostic of the disease. Also claimed are: method (M2) for distinguishing between normal and disease tissues; method (M3) for monitoring the response of a breast cancer patient to treatment with an anti-cancer agent; method (M4) for identifying a compound for treating breast cancer; and an array for distinguishing between normal and disease tissues comprising two or more probes corresponding to genes selected from ADR98995-ADR99121 or comprising two or more polypeptides selected from ADR98995-ADR99121. In M1 and M2 the genes are selected from ADR98995-ADR99121 and the gene products are polypeptides selected from ADR99121-ADR99121. M1 is useful for diagnosing breast cancer. M2 and the array are useful for distinguishing between normal and disease tissue. M3 is useful for monitoring the response of a breast cancer patient to treatment with an anti-cancer agent. M4 is useful for identifying a compound for treating breast cancer. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WFO at ftp.wipo.int/pub/published_pat_sequences.

Sequence 538 AA;

Query Match 100.0%; Score 2787; DB 8; Length 538;

Best Local Similarity 100.0%; Pred. No. 4.2e-244;

Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MEEVNOQPLNEKQIANSQDGYVQVDMNRLHFLCGSGGTYTYIEQKLGLENAA 60
DB 1 MEEVNOQPLNEKQIANSQDGYVQVDMNRLHFLCGSGGTYTYIEQKLGLENAA 60
QY 61 LIRLEDGRCGVIOEIKSFSGEGRTTQOEPMFLALITCSQSDISTKQAKRAVSEVR 120
DB 61 LIRLEDGRCGVIOEIKSFSGEGRTTQOEPMFLALITCSQSDISTKQAKRAVSEVR 120
QY 121 IPTHFTFIOFKKDLKESMKCGMGGALAKALADWNEKGMAALAVTKYQORNGMSHK 180
DB 121 IPTHFTFIOFKKDLKESMKCGMGGALAKALADWNEKGMAALAVTKYQORNGMSHK 180
QY 121 IPTHFTFIOFKKDLKESMKCGMGGALAKALADWNEKGMAALAVTKYQORNGMSHK 180
DB 121 IPTHFTFIOFKKDLKESMKCGMGGALAKALADWNEKGMAALAVTKYQORNGMSHK 180
QY 181 DILRLSHLKPSSBGLAVTKYITTKGKEVHELYKEKALSVETEKILKYLEAVEKVKRTD 240
DB 181 DILRLSHLKPSSBGLAVTKYITTKGKEVHELYKEKALSVETEKILKYLEAVEKVKRTD 240
QY 241 ELEVIHLIEBHLVREHLLTNHLKSKVWKALLOEMLTALLRNIGKMTANSVLEBGNSE 300
DB 241 ELEVIHLIEBHLVREHLLTNHLKSKVWKALLOEMLTALLRNIGKMTANSVLEBGNSE 300
QY 301 VSLVCEKLCNEKLLKKARLHPHILLALFTYKTHGRLGKLKWRPDEBILKALDAAFYKT 360
DB 301 VSLVCEKLCNEKLLKKARLHPHILLALFTYKTHGRLGKLKWRPDEBILKALDAAFYKT 360
QY 361 FKTVEPTGKRFLLADVVSASMNQVLSILNASTVAAMCMVVTREKDSYVVAFSDEVY 420
DB 361 FKTVEPTGKRFLLADVVSASMNQVLSILNASTVAAMCMVVTREKDSYVVAFSDEVY 420
QY 421 PCPVTTDMTLQOVLAMSGQIPAGTTCSPMTIAOCTNPADVFIPTNEFPAGGVHRA 480
DB 421 PCPVTTDMTLQOVLAMSGQIPAGTTCSPMTIAOCTNPADVFIPTNEFPAGGVHRA 480
QY 481 IALREYRKQMDIPAKLIVCGMTSNGFTIADPDRGMLDMCGFPYCALDVIRNFTLDMI 538
DB 481 IALREYRKQMDIPAKLIVCGMTSNGFTIADPDRGMLDMCGFPYCALDVIRNFTLDMI 538

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RESULT 3

AAB46827

ID AAB46827 standard; protein; 552 AA.

XX AAB46827;

XX 26-APR-2001 (first entry)

XX Human antigen SSA60 M4-C6 protein.

XX Antigen, human; SSA60; ribonucleoprotein; autoimmune disease; diagnosis;

XX lupus erythematosus; Sjorgen's syndrome A.

XX Homo sapiens.
OS DE19931380-A1.
XX 11-JAN-2001.
XX 07-JUL-1999; 99DE-01031380.
XX 07-JUL-1999; 99DE-01031380.
XX 07-JUL-1999; 99DE-01031380.
XX (HOF) HOFMANN LA ROCHE & CO AG F.
XX Burckhardt J, Haase M, Lehmann H;
XX WPI, 2001-148274/16.
XX Recombinant production of ribonucleoprotein, useful for diagnosis of
XX autoimmune disease, by expressing, in prokaryotes, sequences encoding
XX both RNA and protein components.

Example 1; Page 13-15; 36pp; German.

This invention describes a novel method for the recombinant production of ribonucleoprotein (I) which comprises producing a prokaryotic host cell that contains at least one DNA (II) encoding an RNA component of (I) and at least one DNA (III) encoding a protein component of (I), expressing both DNAs and then recovering (I). The invention also describes (1) CC nucleic acid constructs containing (II) and (III); (2) recombinant CC prokaryotic cell containing (II) and (III); (3) (I) produced by the new method; and (4) SSA60 protein, designated M56, having a 553 amino acid (aa) sequence, given in the specification, optionally in association with RNA. (I) are used for diagnosis/prognosis of autoimmune diseases, by CC especially systemic lupus erythematosus or Sjorgen's syndrome A, by CC complex formation with (I)-specific antibodies. (I) are produced simply, CC inexpensively and on a large scale, in a functional immunologically CC active form that provides a reliable diagnostic test. Complete (I) are CC more selective and sensitive than the protein component used alone, CC whether recombinant or isolated from bovine spleen

Sequence 552 AA;

Query Match 100.0%; Score 2787; DB 4; Length 552;

Best Local Similarity 100.0%; Pred. No. 4.4e-244;

Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MEEVNOQPLNEKQIANSQDGYVQVDMNRLHFLCGSGGTYTYIEQKLGLENAA 60
DB 1 MEEVNOQPLNEKQIANSQDGYVQVDMNRLHFLCGSGGTYTYIEQKLGLENAA 72
QY 61 LIRLEDGRCGVIOEIKSFSGEGRTTQOEPMFLALITCSQSDISTKQAKRAVSEVR 120
DB 61 LIRLEDGRCGVIOEIKSFSGEGRTTQOEPMFLALITCSQSDISTKQAKRAVSEVR 132
QY 73 LIRLEDGRCGVIOEIKSFSGEGRTTQOEPMFLALITCSQSDISTKQAKRAVSEVR 132
DB 73 LIRLEDGRCGVIOEIKSFSGEGRTTQOEPMFLALITCSQSDISTKQAKRAVSEVR 132
QY 121 IPTHFTFIOFKKDLKESMKCGMGGALAKALADWNEKGMAALAVTKYQORNGMSHK 180
DB 121 IPTHFTFIOFKKDLKESMKCGMGGALAKALADWNEKGMAALAVTKYQORNGMSHK 192
QY 133 IPTHFTFIOFKKDLKESMKCGMGGALAKALADWNEKGMAALAVTKYQORNGMSHK 192
DB 133 IPTHFTFIOFKKDLKESMKCGMGGALAKALADWNEKGMAALAVTKYQORNGMSHK 240
QY 181 DILRLSHLKPSSBGLAVTKYITTKGKEVHELYKEKALSVETEKILKYLEAVEKVKRTD 240
DB 181 DILRLSHLKPSSBGLAVTKYITTKGKEVHELYKEKALSVETEKILKYLEAVEKVKRTD 252
QY 193 DILRLSHLKPSSBGLAVTKYITTKGKEVHELYKEKALSVETEKILKYLEAVEKVKRTD 252
DB 193 DILRLSHLKPSSBGLAVTKYITTKGKEVHELYKEKALSVETEKILKYLEAVEKVKRTD 300
QY 241 ELEVIHLIEBHLVREHLLTNHLKSKVWKALLOEMLTALLRNIGKMTANSVLEBGNSE 300
DB 241 ELEVIHLIEBHLVREHLLTNHLKSKVWKALLOEMLTALLRNIGKMTANSVLEBGNSE 312
QY 301 VSLVCEKLCNEKLLKKARLHPHILLALFTYKTHGRLGKLKWRPDEBILKALDAAFYKT 360
DB 301 VSLVCEKLCNEKLLKKARLHPHILLALFTYKTHGRLGKLKWRPDEBILKALDAAFYKT 372
QY 313 VSLVCEKLCNEKLLKKARLHPHILLALFTYKTHGRLGKLKWRPDEBILKALDAAFYKT 372
DB 313 VSLVCEKLCNEKLLKKARLHPHILLALFTYKTHGRLGKLKWRPDEBILKALDAAFYKT 420
QY 361 FKTVEPTGKRFLLADVVSASMNQVLSILNASTVAAMCMVVTREKDSYVVAFSDEVY 420
DB 361 FKTVEPTGKRFLLADVVSASMNQVLSILNASTVAAMCMVVTREKDSYVVAFSDEVY 432

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QY 421 PCPTTDMTLQOVLMAMSOIPAGGTDCLPMIWAQKNTTPADVFIIVFTDNETFAGVHPA 480
DB 433 PCPTTDMTLQOVLMAMSOIPAGGTDCLPMIWAQKNTTPADVFIIVFTDNETFAGVHPA 492
QY 481 IALREYRKMDIPAKLIYCGMTSNGFTIADPDRGMLDMCGFDTGALDVIRNFTLDM 538
DB 493 IALREYRKMDIPAKLIYCGMTSNGFTIADPDRGMLDMCGFDTGALDVIRNFTLDM 550

RESULT 4
AAB46829 ID AAB46829 standard; protein; 553 AA.
AC AAB46829;
XX
XX 26-APR-2001 (first entry)
XX
XX Human antigen construct pEQ30-HY3-SSA60W56 #4 protein.
XX
XX Antigen; human; SSA60; ribonucleoprotein; autoimmune disease; diagnosis;
KM lupus erythematosus; Sjoergen's syndrome A.
XX
XX Homo sapiens.
OS
XX DE19931380-A1.
PN
XX 11-JAN-2001.
PD
XX
XX 07-JUL-1999; 99DE-01031380.
PP
XX
XX 07-JUL-1999; 99DE-01031380.
PR
XX
XX (HOFF ) HOFFMANN LA ROCHE & CO AG F.
PA
XX Burkhardt J, Haase M, Lehmann H;
PI
XX WPI; 2001-148274/16.
DR N-PSDB; AAF26157.
XX
XX Recombinant production of ribonucleoprotein, useful for diagnosis of
PT autoimmune disease, by expressing, in prokaryotes, sequences encoding
PT both RNA and protein components.
XX
XX Example 1; Page 22-24; 36pp; German.
PS
XX
XX This invention describes a novel method for the recombinant production of
CC ribonucleoprotein (I) which comprises producing a prokaryotic host cell
CC that contains at least one DNA (II) encoding an RNA component of (I) and
CC at least one DNA (III) encoding a protein component of (I), expressing
CC both DNAs and then recovering (I). The invention also describes (1)
CC nucleic acid constructs containing (II) and (III); (2) recombinant
CC prokaryotic cell containing (II) and (III); (3) (I) produced by the new
CC method; and (4) SSA60 protein, designated M56, having a 553 amino acid
CC (aa) sequence, given in the specification, optionally in association with
CC RNA. (I) are used for diagnosis/prognosis of autoimmune diseases,
CC especially systemic lupus erythematosus or Sjoergen's syndrome A, by
CC complex formation with (I)-specific antibodies. (I) are produced simply,
CC inexpensively and on a large scale, in a functional (immunologically
CC active) form that provides a reliable diagnostic test. Complete (I) are
CC more selective and sensitive than the protein component used alone,
CC whether recombinant or isolated from bovine spleen
XX
XX Sequence 553 AA;
SQ
Query Match 99.8%; Score 2782; DB 4; Length 553;
Best Local Similarity 100.0%; Pred. No. 1,3e-243;
Matches 537; Conservativity 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 EESVNOQOPLNEKQIANSQDGYVQVTDNMLRHLPLCGSGGTYIYKEQGLGENABAL 61
DB 17 EESVNOQOPLNEKQIANSQDGYVQVTDNMLRHLPLCGSGGTYIYKEQGLGENABAL 76

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QY 62 IRLIEDRGCEVIOEIKSFQEGRTTKQEBMFLPALAICSCQSDISTKQAFKAVSEVCRI 121
DB 77 IRLIEDRGCEVIOEIKSFQEGRTTKQEBMFLPALAICSCQSDISTKQAFKAVSEVCRI 136
QY 122 PTHLFTFIQPKKOLKESMKCGMGRALRKALADWYNEKGMALALAVTKYKQNRGSHKD 181
DB 137 PTHLFTFIQPKKOLKESMKCGMGRALRKALADWYNEKGMALALAVTKYKQNRGSHKD 196
QY 182 LRLSHLKPSSEGLAVYTKYITKGWKEVHELYEKLVSFTEKLLKYLAVKVKRTKDE 241
DB 197 LRLSHLKPSSEGLAVYTKYITKGWKEVHELYEKLVSFTEKLLKYLAVKVKRTKDE 256
QY 242 LEVYHLIEBHRVLRHLLTNHLKSKEVWKALLQEMPLTALLRNIGKXTANSVLBPGNSEV 301
DB 257 LEVYHLIEBHRVLRHLLTNHLKSKEVWKALLQEMPLTALLRNIGKXTANSVLBPGNSEV 316
QY 302 SLVCEKLCNEKLLKARIRHFFHLLALEYTKYTGHGRLKMRPDEEILKALDAAFYKTF 361
DB 317 SLVCEKLCNEKLLKARIRHFFHLLALEYTKYTGHGRLKMRPDEEILKALDAAFYKTF 376
QY 362 KTVBPTGKRFLAVDVASANNORVLGSLINASTVVAAMCMVVRTEKDSYVAFPSDEMVP 421
DB 377 KTVBPTGKRFLAVDVASANNORVLGSLINASTVVAAMCMVVRTEKDSYVAFPSDEMVP 436
QY 422 CPVTTDMTLQOVLMAMSOIPAGGTDCLPMIWAQKNTTPADVFIIVFTDNETFAGVHPA 481
DB 437 CPVTTDMTLQOVLMAMSOIPAGGTDCLPMIWAQKNTTPADVFIIVFTDNETFAGVHPA 496
QY 482 ALREYRKMDIPAKLIYCGMTSNGFTIADPDRGMLDMCGFDTGALDVIRNFTLDM 538
DB 497 ALREYRKMDIPAKLIYCGMTSNGFTIADPDRGMLDMCGFDTGALDVIRNFTLDM 553

RESULT 5
AAB46828 ID AAB46828 standard; protein; 553 AA.
XX
XX AAB46828;
XX
XX 26-APR-2001 (first entry)
DT
XX
XX Human antigen SSA60 M56 protein.
DE
XX
XX Antigen; human; SSA60; ribonucleoprotein; autoimmune disease; diagnosis;
KM lupus erythematosus; Sjoergen's syndrome A.
XX
XX Homo sapiens.
OS
XX DE19931380-A1.
PN
XX 11-JAN-2001.
PD
XX
XX 07-JUL-1999; 99DE-01031380.
PP
XX
XX 07-JUL-1999; 99DE-01031380.
PR
XX
XX (HOFF ) HOFFMANN LA ROCHE & CO AG F.
PA
XX Burkhardt J, Haase M, Lehmann H;
PI
XX WPI; 2001-148274/16.
DR
XX
XX Recombinant production of ribonucleoprotein, useful for diagnosis of
PT autoimmune disease, by expressing, in prokaryotes, sequences encoding
PT both RNA and protein components.
XX
XX Claim 15; Page 15-18; 36pp; German.
PS
XX
XX This invention describes a novel method for the recombinant production of
CC ribonucleoprotein (I) which comprises producing a prokaryotic host cell
CC that contains at least one DNA (II) encoding an RNA component of (I) and
CC at least one DNA (III) encoding a protein component of (I), expressing
CC both DNAs and then recovering (I). The invention also describes (1)

```

CC nucleic acid constructs containing (II) and (III); (2) recombinant
 CC prokaryotic cell containing (II) and (III); (3) (I) produced by the new
 CC method; and (4) SSA60 protein, designated M56, having a 553 amino acid
 CC (aa) sequence, given in the specification, optionally in association with
 CC RNA. (I) are used for diagnosis/prognosis of autoimmune diseases,
 CC especially systemic lupus erythematosus or Sjogren's syndrome A, by
 CC complex formation with (I)-specific antibodies; (I) are produced simply,
 CC inexpensively and on a large scale, in a functional (immunologically
 CC active) form that provides a reliable diagnostic test. Complete (I) are
 CC more selective and sensitive than the protein component used alone,
 CC whether recombinant or isolated from bovine spleen

XX Sequence 553 AA;

Query Match 99.8%; Score 2782; DB 4; Length 553;
 Best Local Similarity 100.0%; Pred. No. 1.3e-243;
 Matches 537; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EESVYVQMPLEKQJANSQDGVWQVDMRLHRLFCGSGGGTYYIEQKLGLENMAL 61
 DB 17 EESVYVQMPLEKQJANSQDGVWQVDMRLHRLFCGSGGGTYYIEQKLGLENMAL 76
 QY 62 IRLLEDGCGCEVIOEIKSFSGEGRTTKQBPMLFALATGSCSDISTKQAFKAVSEVCRI 121
 DB 77 IRLLEDGCGCEVIOEIKSFSGEGRTTKQBPMLFALATGSCSDISTKQAFKAVSEVCRI 136
 QY 122 PTHLFTFQPKKDLKESMKCGMGRALKALADWTNKGGMALALAVTKYKQRMGMSHKD 181
 DB 137 PTHLFTFQPKKDLKESMKCGMGRALKALADWTNKGGMALALAVTKYKQRMGMSHKD 196
 QY 182 LLRLSHLKPSSEGLAVITKYYTKGKEVHELYKEKALSVETBKILKYIEAVEKVKRTQDE 241
 DB 197 LLRLSHLKPSSEGLAVITKYYTKGKEVHELYKEKALSVETBKILKYIEAVEKVKRTQDE 256
 QY 242 LEVHLIEEHLVREHLTLTNLKSKEWKALLOEMLFALLRNIGKMTANSVLEPENSEV 301
 DB 257 LEVHLIEEHLVREHLTLTNLKSKEWKALLOEMLFALLRNIGKMTANSVLEPENSEV 316
 QY 302 SLVECKLCNEKLLKARLHPHILLALETKYTGHLRGKILKMRPDEILKALDAAFYKTF 361
 DB 317 SLVECKLCNEKLLKARLHPHILLALETKYTGHLRGKILKMRPDEILKALDAAFYKTF 376
 QY 362 KTVBPTGGRFLIADVSAWNOVIGSILNASTVAAMCMVTTRREKOSYVAEDEVNP 421
 DB 377 KTVBPTGGRFLIADVSAWNOVIGSILNASTVAAMCMVTTRREKOSYVAEDEVNP 436
 QY 422 CPVTTDMTLQOVLAMSGQIPAGGTCSLPMIWAQKTNTPADVFIYFTDNETPAGGVHPAI 481
 DB 437 CPVTTDMTLQOVLAMSGQIPAGGTCSLPMIWAQKTNTPADVFIYFTDNETPAGGVHPAI 496
 QY 482 ALREYRKQMDIPAKLIVCGMTSNGFTIADPDDRGMLDMCGFPTGALADVIRNFTLMI 538
 DB 497 ALREYRKQMDIPAKLIVCGMTSNGFTIADPDDRGMLDMCGFPTGALADVIRNFTLMI 553

RESULT 6

ADRA1766 standard; protein; 525 AA.

ADRA1766;

21-OCT-2004 (first entry)

Protein sequence of human SS-A/Ro ribonucleoprotein 60 kD autoantigen.

XX Human, autoantigen; SS-A/Ro ribonucleoprotein; SS-A;
 KM notch signalling pathway; autoimmune disorder; bystander effect;
 KM suppression; DSL domain; EGF domain; Goodpasture's disease;
 KM Wegener's granulomatosis; anaemia; thrombocytopenia; gastritis;
 KM hepatitis; vasculitis; scleroderma; myositis; arthritis;
 KM systemic lupus erythematosus; SLE; Sjogren's syndrome; hepatic fibrosis;
 KM liver cirrhosis; thyroiditis; dermatitis; placental dysfunction;
 KM eclampsia; inflammatory related gynaecological disease;

KM neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
 KM Huntington disease; encephalitis; psychiatric disorder; Down's syndrome;
 KM stroke; exogenous; bystander antigen; multiple sclerosis;
 KM delta serrate leg; inflammatory bowel disease; notch receptor.

OS Homo sapiens.

XX WO2004064863-A1.

XX 05-AUG-2004.

XX 23-JAN-2004; 2004WO-GB000263.

XX 23-JAN-2003; 2003GB-00001510.
 PR 23-JAN-2003; 2003GB-00001512.
 PR 23-JAN-2003; 2003GB-00001513.
 PR 23-JAN-2003; 2003GB-00001515.
 PR 23-JAN-2003; 2003GB-00001518.
 PR 23-JAN-2003; 2003GB-00001519.
 PR 23-JAN-2003; 2003GB-00001521.
 PR 23-JAN-2003; 2003GB-00001522.
 PR 23-JAN-2003; 2003GB-00001524.
 PR 23-JAN-2003; 2003GB-00001526.
 PR 23-JAN-2003; 2003GB-00001527.
 PR 23-JAN-2003; 2003GB-00001529.
 PR 04-APR-2003; 2003WO-GB001525.
 PR 24-MAY-2003; 2003GB-00012062.
 PR 01-AUG-2003; 2003WO-GB003285.
 PR 03-OCT-2003; 2003GB-00023130.
 PR 07-JAN-2004; 2004WO-GB000046.

XX (LORA-) LORANTIS LTD.

XX Champion BR, Ragno S, Young LL;

XX WPI, 2004-562091/54.

XX New product having a modulator of the Notch signalling pathway, useful for
 PT modulating an immune response in autoimmune disorders, such as anaemia,
 PT gastritis, hepatitis, scleroderma and myositis.

PS Disclosure; Page 112-113; 244pp; English.

XX The invention relates to the modulation of immune function through a
 CC notch signalling pathway for the prevention of autoimmune diseases. It
 CC has been found that the notch signalling pathway provides a bystander
 CC effect or bystander suppression effect, which can be used in a wide
 CC variety of ways to suppress unwanted immune responses in immune diseases
 CC and disorders. Autoimmune diseases are characterised by immune responses
 CC that are directed against self antigens. T lymphocytes are activated upon
 CC recognition of a self antigen and/or a foreign antigen as a complex with
 CC self major histocompatibility complex (MHC) gene products on the surface
 CC of antigen presenting cells (APC). The invention provides the method of
 CC modulating of an immune response, modulator information and a
 CC pharmaceutical kit for suppression of an immune response. The modulator
 CC of the notch signalling pathway is an agent which activates the notch
 CC receptor or a polynucleotide which codes for such an agent. It comprises
 CC a protein or polypeptide comprising a notch ligand DSL (delta serrate
 CC lag) domain, notch ligand EGF domain, optionally all or part of a notch
 CC ligand N terminal domain, and optionally one or more heterologous amino
 CC acid or a polynucleotide sequences. The modulator can be a fusion protein
 CC comprising a segment of a notch ligand extracellular domain and an
 CC immunoglobulin Fc segment. The disorders include Goodpasture's disease,
 CC Wegener's granulomatosis, autoimmune anaemia, thrombocytopenia,
 CC gastritis, autoimmune hepatitis, inflammatory bowel disease, autoimmune
 CC vasculitis, scleroderma, myositis, autoimmune arthritis, Systemic Lupus
 CC erythematosus (SLE) or Sjogren's syndrome, hepatic fibrosis, liver
 CC cirrhosis, thyroiditis, dermatitis, placental dysfunction, eclampsia,
 CC inflammatory related gynaecological diseases, neurodegenerative disorders
 CC (such as Alzheimer's disease, Parkinson's disease, Huntington disease)
 CC encephalitis, psychiatric disorders, Down's syndrome, stroke, multiple
 CC sclerosis, etc. The invention discloses a method for generating immune
 CC suppression at a disease locus by administering an exogenous antigen. It

also provides the use of modulator or activator of notch signaling in simultaneous, separate or sequential combination with a bystander antigen or antigenic determinant for reducing an immune response to a target antigen. The presented protein sequence is the human SS-A/Ro ribonucleoprotein autoantigen (60 kD) which is an example of Sjogren's syndrome autoantigen and bystander antigen.

SQ **Sequence 525 AA;**

Query Match	95.4%	Score 2659;	DB 8;	Length 525;
Best Local Similarity	99.4%	Pred. No. 1.8e-22;		
Matches 513; Conservative	2;	Mismatches 1;	Indels 0;	Gaps 0;

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QY 1 MEESNOMQPLNEKQJANSODGVYVOTVMTNRLHRLCGSEBEGTYYIKKQJGLENAEA 60
Db 1 MEESNOMQPLNEKQJANSODGVYVOTVMTNRLHRLCGSEBEGTYYIKKQJGLENAEA 60
QY 61 LIRLJEDGRCVEIJOEIKSFQEGRTTQKQPMFLALICQSCSDISTKQAFRAVSEVCR 120
Db 61 LIRLJEDGRCVEIJOEIKSFQEGRTTQKQPMFLALICQSCSDISTKQAFRAVSEVCR 120
QY 121 IPTHLPFLOPKKDXKESMKCGMWGALRRKALIDWNEKGMALALAVTYKORNGMSHK 180
Db 121 IPTHLPFLOPKKDXKESMKCGMWGALRRKALIDWNEKGMALALAVTYKORNGMSHK 180
QY 181 DLRLSHLKPSSEBGALIVKYIIRKQKEVHELKEXALSVETEKLLKYLEAVEKVYKTXD 240
Db 181 DLRLSHLKPSSEBGALIVKYIIRKQKEVHELKEXALSVETEKLLKYLEAVEKVYKTXD 240
QY 241 ELEVLHLEBHLVREHLLTNHLSKSEWPKALLQEMPLTLLANLIGMTNANSLBEPNSE 3000
Db 241 ELEVLHLEBHLVREHLLTNHLSKSEWPKALLQEMPLTLLANLIGMTNANSLBEPNSE 3000
QY 301 VSLVCEKLCNEKLLKKARLHPFILLALBETYKTHGHLRGKLRPDEILKALDAAFYKT 360
Db 301 VSLVCEKLCNEKLLKKARLHPFILLALBETYKTHGHLRGKLRPDEILKALDAAFYKT 360
QY 361 FKTVEPTGRFLIANDVSAANORVUGSILINASTVAAAMCMVYTRPKDSYVVAFSPEMV 420
Db 361 FKTVEPTGRFLIANDVSAANORVUGSILINASTVAAAMCMVYTRPKDSYVVAFSPEMV 420
QY 421 PCPVTTDMTLOQVILAMSOI PAGTDCSLPMIAOKNTPEADVIFYETDNETAGGVHFA 480
Db 421 PCPVTTDMTLOQVILAMSOI PAGTDCSLPMIAOKNTPEADVIFYETDNETAGGVHFA 480
QY 481 IALREYRKMDIPAKLIVCGMNSGPTIADPDRGM 516
Db 481 IALREYRKMDIPAKLIVCGMNSGPTIADPDRAL 516

```

DT	16-DEC-2004 (first entry)
XX	
DE	Human SS-A/Ro ribonucleoprotein autoantigen 60 kD subunit.

KM Cytostatic; Immunosuppressive; Antidiabetic; Neutroprotective;
KM Antiarrhythmic; Antineumatic; Antiallergic; Vaccine; Notch signaling;
KM Notch; Notch ligand; Delta protein; Serrate protein; Jagged protein;
KM multiple sclerosis; rheumatoid arthritis; diabetes; allergy;
KM immune disorder; autoimmune disease; graft rejection; cancer;
KM organ transplant; human; Sjogren's syndrome; SS-A;
KM Ro ribonucleoprotein autoantigen 60 kD subunit.

OS	Homo sapiens.
XX	
PN	WO2004083372-A2.
XX	
4PD	30-SEP-2004.

XX 22-MAR-2004; 2004WO-GB001229.
PF XX
PR 21-MAR-2003; 2003GB-00006582.
PR 21-MAR-2003; 2003GB-00006583.
PR 22-MAR-2003; 2003GB-00006621.
PR 22-MAR-2003; 2003GB-00006622.
PR 22-MAR-2003; 2003GB-00006624.
PR 22-MAR-2003; 2003GB-00006626.
PR 22-MAR-2003; 2003GB-00006640.
PR 22-MAR-2003; 2003GB-00006644.
PR 22-MAR-2003; 2003GB-00006650.
PR 22-MAR-2003; 2003GB-00006651.
PR 22-MAR-2003; 2003GB-00006654.

PI Champion BR, Ragno S;
XX
DR WPI, 2004-709927/69.
XX
PT Particle capable of being inserted into or taken up by cell useful for
PT modulating immune response to antigen in subject, comprises
PT polynucleotide coding for modulator of Notch signaling, and
PT polynucleotide coding for antigen.

PS Disclosure: Page 162; 278pp; English.

XX The present invention relates to a particle (1) capable of being inserted
CC into or taken up by a cell comprising (1) a polynucleotide coding for a
CC modulator of Notch signaling, and (1i) a polynucleotide coding for an
CC antigen or antigenic determinant. The first polynucleotide sequence codes
CC for a Notch ligand such as a Delta or Serrate/Jagged protein or its
CC fragment, derivative, homologue, analogue or allelic variant, or for a
CC protein which comprises a Notch ligand DSL domain and at least one Notch
CC ligand EGF-like domain and optionally a membrane binding or transmembrane
CC domain. The first and second sequences are operably linked to one or more
CC promoters or enhancers or polyadenylation sequences. The antigen or
CC antigenic determinant is an allergen, autoantigen, Major
CC histocompatibility complex (MHC) (transplant) antigen, pathogen antigen,
CC tumour antigen or their antigenic determinant. (1i) is useful for
CC modulating an immune response to an antigen in a subject. Pharmaceutical
CC compositions comprising (1) are useful for treating or preventing
CC conditions mediated by T cells, such as multiple sclerosis, rheumatoid
CC arthritis, diabetes, allergy, for treating immune disorders such as
CC autoimmune diseases of graft rejection such as allograft rejection,
CC treating cancer and organ transplants. The present sequence is human SS-
CC A/Ro ribonucleoprotein autoantigen 60 kD subunit which is an autoantigen
CC involved in Sjogren's syndrome and can be used as an antigen to prepare
CC the particle of the invention.

Query Match	95.4%	Score 2659;	DB 8;	Length 525;
Best Local Similarity	99.4%;	Pred. No. 1.8e-232;		
Matches 513; Conservative	2;	Mismatches 1;	Indels 0;	Gaps 0;

QY	1	MEESVNQOPIANEKQIANSODGYWQUTDMNRHRLPFCFSGEGTYYIKKQKGLIENEA	60
Db	1	MEESVNQOPIANEKQIANSODGYWQUTDMNRHRLPFCFSGEGTYYIKKQKGLIENEA	60
QY	61	LIRLEEDRGCEVIOEIKSFQEGRTTKQBPMLFALICSGCSDISTKQAFKAVSEYCR	120
Db	61	LIRLEEDRGCEVIOEIKSFQEGRTTKQBPMLPALICSGCSDISTKQAFKAVSEYCR	120
QY	121	IPTHLFETIOFKDOKESMCGMMGRALRKAIADWYNEKGMALALAVTKYKÖRNGSMHK	180
Db	121	IPTHLFETIOFKDOKESMCGMMGRALRKAIADWYNEKGMALALAVTKYKÖRNGSMHK	180
QY	161	DILRLSHUKPESSEGAIATYKTIITGMEVHELYEKAALSVTEBQLKLTLEAVERYKRPKD	240
Db	161	DILRLSHUKPESSEGAIATYKTIITGMEVHELYEKAALSVTEBQLKLTLEAVERYKRPKD	240

QY 241 ELEVTNHLIEBRLVREHLITNHLKSEYWKALLQEMPTALLRNIGKMTANSVLEBGNSE 300
 DB 241 ELEVTNHLIEBRLVREHLITNHLKSEYWKALLQEMPTALLRNIGKMTANSVLEBGNSE 300
 QY 301 VSLVCEKLCNEKLLKKARLHPHILIALETYKTGHLGKGLKMRPDEELIKALDAAFYKT 360
 DB 301 VSLVCEKLCNEKLLKKARLHPHILIALETYKTGHLGKGLKMRPDEELIKALDAAFYKT 360
 QY 361 FKTVBPTGKRFLLAVDVASASNNQVLSILNASTVAAACMVVTRTEKOSYVAFSDMV 420
 DB 361 FKTVBPTGKRFLLAVDVASASNNQVLSILNASTVAAACMVVTRTEKOSYVAFSDMV 420
 QY 421 PCPVTDTMTLQOVLMAASQIPAGGTDGSLPMIWAOKTNPADVFIYFTDNETPAGGVH 480
 DB 421 PCPVTDTMTLQOVLMAASQIPAGGTDGSLPMIWAOKTNPADVFIYFTDNETPAGGVH 480
 QY 481 IALREYRKMDIPAKLIVCGMTSNGFTIADPDDRG 516
 DB 481 IALREYRKMDIPAKLIVCGMTSNGFTIADPDDRG 516

RESULT 8

AAM03717
 ID AAM03717 standard; protein; 413 AA.

AC AAM03717,
 DT 25-MAR-2003 (revised)
 DT 12-MAR-1997 (first entry)
 DE Human autoantigen Ro(SS-A).
 XX Autoimmune disease; Ia autoantigen; Sjogren's syndrome;
 XX systemic lupus erythematosus; diagnosis.
 OS Homo sapiens.

FH Key Location/Qualifiers
 FT 1. 413
 FT /label= Ro antigen
 FT /note= "X's in the present sequence indicate amino acid
 FT positions given the designation End in the specification"

PN US5541291-A.
 PD 30-JUL-1996.
 PF 27-MAY-1987; 87US-00054871.
 PR 31-DEC-1984; 84US-00687908.
 PA (UYDU-) UNIV DUKE.

PI Keene JD,
 DR WPI; 1996-362015/36.

PT Auto-antigen U2-RNP, associated with severe polymyositis-scleroderma
 PT overlap syndrome - useful for diagnosis and treatment of autoimmune
 PT diseases.

PS Disclosure; Col 15-16; 21pp; English.

CC The human Ro protein is highly common among autoimmune patients. Ro is
 CC characteristic of patients with Sjogren's syndrome and is likely to be a
 CC major pathogenic factor in the foetal heartblock syndrome. Ro cDNA has
 CC been isolated from a human brain library. (Updated on 25-MAR-2003 to
 CC correct PF field.)

XX Sequence 413 AA;

Query Match 63.8%; Score 1778; DB 2; Length 413;
 Best Local Similarity 96.9%; Pred. No. 1.8e-152;

Matches 349; Conservative 1; Mismatches 6; Indels 4; Gaps 1;
 QY 183 LRLSHKSSSE----GLAIYTKYITTKGKVEHLYKKEALSVEREKLLKYLEAVEKVRT 238
 DB 13 LILRLRBRGRLPQTGLAIVTKYITTKGKVEHLYKKEALSVEREKLLKYLEAVEKVRT 72
 QY 239 KOELEVTNHLIEBRLVREHLITNHLKSEYWKALLQEMPTALLRNIGKMTANSVLEBGN 298
 DB 73 KOELEVTNHLIEBRLVREHLITNHLKSEYWKALLQEMPTALLRNIGKMTANSVLEBGN 132
 QY 299 SEVSIVCEKLCNEKLLKKARLHPHILIALETYKTGHLGKGLKMRPDEELIKALDAAFY 358
 DB 133 SEVSIVCEKLCNEKLLKKARLHPHILIALETYKTGHLGKGLKMRPDEELIKALDAAFY 192
 QY 359 KTFKTVBPTGKRFLLAVDVASASNNQVLSILNASTVAAACMVVTRTEKOSYVAFSD 418
 DB 193 KTFKTVBPTGKRFLLAVDVASASNNQVLSILNASTVAAACMVVTRTEKOSYVAFSD 252
 QY 419 MWPCTVDTMTLQOVLMAASQIPAGGTDGSLPMIWAOKTNPADVFIYFTDNETPAGGVH 478
 DB 253 MWPCTVDTMTLQOVLMAASQIPAGGTDGSLPMIWAOKTNPADVFIYFTDNETPAGGVH 312
 QY 479 PALALREYRKMDIPAKLIVCGMTSNGFTIADPDDRGMLDMCGFDYALDVIRNFTLDM 538
 DB 313 PALALREYRKMDIPAKLIVCGMTSNGFTIADPDDRGMLDMCGFDYALDVIRNFTLDM 372

RESULT 9

AAB94864
 ID AAB94864 standard; protein; 557 AA.

AC AAB94864;
 DT 26-JUN-2001 (first entry)

DE Human protein sequence SEQ ID NO:16064.

XX Human; primer; detection; diagnosis; antisense therapy; gene therapy.

XX Homo sapiens.

XX EP1074617-A2.

XX 07-FEB-2001.

XX 28-JUL-2000; 2000EP-00116126.

XX 29-JUL-1999; 99JP-00248036.

XX 27-AUG-1999; 99JP-00300253.

XX 11-JAN-2000; 2000JP-00118776.

XX 02-MAY-2000; 2000JP-00183767.

XX 09-JUN-2000; 2000JP-00241899.

XX (HELI-) HELIX RES INST.

XX Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;

XX Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;

XX WPI; 2001-318749/34.

XX Claim 8; SEQ ID NO 16064; 2537bp + Sequence Listing; English.

CC The present invention describes primer sets for synthesizing 5602 full-
 CC length cDNAs defined in the specification. Where a primer set comprises:
 CC (a) an oligo-dT primer and an oligonucleotide complementary to the
 CC complementary strand of a polynucleotide which comprises one of the 5602
 CC nucleotide sequences defined in the specification, where the
 CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination

CC of an oligonucleotide comprising a sequence complementary to the
 CC complementary strand of a polynucleotide which comprises a 5'-end
 CC sequence and an oligonucleotide comprising a sequence complementary to a
 CC polynucleotide which comprises a 3'-end sequence, where the
 CC oligonucleotide comprises at least 15 nucleotides and the combination of
 CC the 5'-end sequence/3'-end sequence is selected from those defined in the
 CC specification. The primer sets can be used in antisense therapy and in
 CC gene therapy. The primers are useful for synthesizing polynucleotides,
 CC particularly full-length cDNAs. The primers are also useful for the
 CC detection and/or diagnosis of the abnormality of the proteins encoded by
 CC the full-length cDNAs. The primers allow obtaining of the full-length
 CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
 CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893
 CC represent human amino acid sequences, and AAH13629 to AAH13632 represent
 CC oligonucleotides, all of which are used in the exemplification of the
 CC present invention

XX
 SQ Sequence 557 AA;

Query Match 63.4%; Score 1768; DB 4; Length 557;
 Best Local Similarity 99.4%; Pred. No. 2.3e-151;
 Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 194 GLAIVTKYITKGWKEVHELYEKALSVETEKLLKYLBAVEKVKTKDLEVIHLIEEHL 253
 |||||||
 DB 213 GLAIVTKYITKGWKEVHELYEKALSVETEBLLKYLBAVEKVKTRDELVIHLIEEHL 272
 |||||||

QY 254 VREHLITNHLKSKVEWKALLQEMPLTALIRNIGKMTANSVLEPNSVSLVCEKLCNEKL 313
 |||||||
 DB 273 VREHLITNHLKSKVEWKALLQEMPLTALIRNIGKMTANSVLEPNSVSLVCEKLCNEKL 332
 |||||||

QY 314 LKKARIRPHILLALEYTKGHGRGLKMRPDEBELLKALDAFYKTPKVTPEPKRFL 373
 |||||||
 DB 333 LKKARIRPHILLALEYTKGHGRGLKMRPDEBELLKALDAFYKTPKVTPEPKRFL 392
 |||||||

QY 374 AVDVASAMNORVLGSIINASTVAAAMCVVTRTEKDSVVAFSDEMPVCPVTDTMTLQOV 433
 |||||||
 DB 393 AVDVASAMNORVLGSIINASTVAAAMCVVTRTEKDSVVAFSDEMPVCPVTDTMTLQOV 452
 |||||||

QY 434 LMAWSQIPAGGTGCSLPMIWAQKNTNPADVIVFTDNETFAGVHPAIALREYRKKMDIP 493
 |||||||
 DB 453 LMAWSQIPAGGTGCSLPMIWAQKNTNPADVIVFTDNETFAGVHPAIALREYRKKMDIP 512
 |||||||

QY 494 AKLIVCGMTSNGFTIADPDDRGMLDMGSPDNGALDIVIRNFTLDM 538
 |||||||
 DB 513 AKLIVCGMTSNGFTIADPDDRGMLDMGSPDNGALDIVIRNFTLDM 557
 |||||||

RESULT 10
 AAY22511
 ID AAY22511 standard; protein; 70 AA.

XX
 AC AAY22511;
 XX
 DT 19-OCT-1999 (first entry)
 DE Human RORNP-60K protein.
 XX
 XX Cognate RNA; gene expression regulator; RNA-protein interaction; UI RNA;
 KM autoimmune disease; neoplastic disease; developmental biology;
 KM RNA-associated protein.
 XX
 OS Homo sapiens.
 XX
 PN US5866680-A.
 PN
 PD 02-FEB-1999.
 PD
 PF 07-JUN-1995; 95US-00474753.
 PF
 PR 15-NOV-1989; 89US-00436779.
 PR 12-JUN-1990; 90US-00536943.
 PR 27-DEC-1993; 93US-00173941.

XX
 PA (KEEN/) KEENE J D.
 PA (OUER/) QUERY C C.
 PA (BENT/) BENTLEY R.
 PI Bentley RO, Keene JD, Query CC;
 DR WPI; 1999-142012/12.
 XX
 PT Conjugates of UI ribonucleoprotein RNA - with nucleic acid probes,
 PT antigens and antibodies.
 XX
 PS Claim 6; Fig 6; 53pp; English.
 XX
 CC This sequence represents an RNA-associated protein. The invention relates
 CC to a compound of formula (IX): (component Y) -(cognate RNA) where:
 CC component Y is covalently bound to the cognate RNA and is selected from
 CC DNA probes, RNA probes, antigens and antibodies; and the cognate RNA is a
 CC polynucleotide comprising at least the sequence shown in AAX84881 and up
 CC to the sequence of UI RNA. The compounds may have a useful application in
 CC numerous fields, including: regulation of gene expression, RNA-protein
 CC interactions, autoimmune and neoplastic diseases, and developmental
 CC biology

XX
 SQ Sequence 70 AA;

Query Match 13.2%; Score 367; DB 2; Length 70;
 Best Local Similarity 98.6%; Pred. No. 2.7e-25;
 Matches 69; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 92 MLFALAIQCSQSDISTKQAFKAVSEVCRIPTHLPTFIQPKDLKESMKCGMGRALRKA 151
 |||||||
 DB 1 MLFKAICSCQSDISTQAFKAVSEVCRIPTHLPTFIQPKDLKESMKCGMGRALRKA 60
 |||||||

QY 152 IADWNEKGG 161
 |||||||
 DB 61 IADWNEKGG 70
 |||||||

RESULT 11
 ABB59719
 ID ABB59719 standard; protein; 641 AA.

XX
 AC ABB59719;
 XX
 DT 26-MAR-2002 (first entry)
 XX
 DE Drosophila melanogaster polypeptide SEQ ID NO 5949.
 XX
 KM Drosophila; developmental biology; cell signalling; insecticide;
 KM pharmaceutical.
 XX
 OS Drosophila melanogaster.
 XX
 PN WO200171042-A2.
 PN
 PD 27-SEP-2001.
 PD
 PF 23-MAR-2001; 2001WO-US009231.
 PF
 PR 23-MAR-2000; 2000US-0191637P.
 PR 11-JUL-2000; 2000US-00614150.
 PR
 PA (PEKE) PE CORP NY.
 PA
 PI Venter JC, Adams M, Li PWD, Myers EW;
 XX WPI; 2001-656860/75.
 DR N-PSDB; ABL03822.
 DR
 PR New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions.

XX Disclosure; SEQ ID NO 5949; 21bp + Sequence Listing; English.
 PS
 CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from *Drosophila*. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (AB16176-AB13511), expressed DNA
 CC sequences (AB101840-AB16175) and the encoded proteins (AB057737-
 CC AB072072). The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at http://wipo.int/pub/published_pcc_sequences

XX
 XX
 SQ Sequence 641 AA;

Query Match 6.7%; Score 185.5; DB 4; Length 641;

Best Local Similarity 19.5%; Pred. No. 2.8e-07; Indels 159; Gaps 28;

Matches 123; Conservative 108; Mismatches 242;

QY 1 MEESVNMQOPLNE---KQIANSQDG-YWQVTDNRHLHFLCFGS-EGGTYYIKQKGL 55
 DB 64 MEKKAISQPLKDESKQEPNSEGTAISTPAIDKLRFRFGSTDEPVYTPALDLYV 123
 QY 56 EN-----AEALIRLIJEDGRCGVIOIRKSF-----SQEGRTTKQZPMFLAICSCSDI 105
 DB 124 ENNPASLKELCQVSED---ELVECLSLVLSGSEPNREQPPRPDEPLILAVFTTCBE 179
 QY 106 SIKQAAFAVAVSEVCIPTHLFTPIQPKDKESM-KCGMGWALKAIDWNEKGML 164
 DB 180 KKNRVNRRFTLTISESDLLFVQLVKKVQKLEKTPENFTRKAVLNMWYTK-SLDR 238
 QY 165 ALAVTKYKORNCW-SHKDLLRLSHLKPSS--EGLAVTKYTKGWKEVH-----L 212
 DB 229 LIHPSIGDGNMPPARLDLYRLHPRNAPLEIIAARLLSSPPELSQWDFLTPLS 298
 QY 213 YKEKALSVETKLLKYLE-AVERKVKTKQDELEVI-HLIEHRLVREHLLTNHLKSKEW 269
 DB 289 PRETIEGVVKKRLTDPBOAIGIVKKLSLSEWHPFHLLHDPRLA--HFLIPHMS----Y 352
 QY 270 KALLQEMPTALLRNIGKNTANSVLEPNSVSVCEKCNKLLKKARIPHILLALE 329
 DB 353 EQLLQKMPRLSRL-----NSRVPRAEQLDKKQLKASNVPRLLLE-- 395
 QY 330 TYKTGHGLRGKLMRPDEILKAL-----DAAFYK-----TFK 362
 DB 396 -----DKRLRKPKYVNVOLVLPSSLKKNTPFKPCATTSFQKASFLHSVEISFG 445
 QY 363 TVEPTGKRPFLAVDVASNMQRVLGSLNAS-----TVAAAMCVTRTEKDSYVAF 415
 DB 446 LNKALGR-----LHITLNEQAVLGKLGSPCRSLKYLDALVALGFGYFRSDRKVTVEFW 501
 QY 416 SD---EMVCPPTTMDTLOOVLMANSQIPAGGDCSLPIMAKNTT----- 459
 DB 502 HDSRGKLKALPWTNMSVSE-----AKTCCB-----NQKVTFNHSPVFTIDIR 546
 QY 460 -----PAVPIPTDNETPAGVHP-----AIALREYRKMDIPAKLIYCGM-- 501
 DB 547 FRALDMDQTFDVLVLPQ--AARGNPNNSKCLAAALMDKREGRANSNAFTIMVSLAQ 603
 QY 502 TSNQFTIADPDRGMLDMCGFDTGALDVI RN F 533
 DB 604 RORSMYSSGRNENMLLECLSDKGTPLINAF 635

RESULT 12

AAR96038

AA96038 standard; protein; 719 AA.

AA96038, (first entry)

XX
 XX
 DT 24-FEB-1997 (first entry)
 XX

DE 80 kD protein.

XX Tetrahymena; 80 kD protein; 95 kD protein; telomerase; telomeric repeat;
 KW RNA coupled protein; chromosome; telomere repeat synthesis; antibody;
 KW immortalised cell; cancer; eukaryotic microbe; inhibitor; gene therapy;
 KW fungal infection; therapy; diagnosis; protozoan infection; somatic cell;
 KW p80; p95.

XX Tetrahymena thermophila.

XX WO9619580-A2.

XX 27-JUN-1996.

XX 18-DEC-1995; 95WO-US016531.

XX 19-DEC-1994; 94US-00359125.

XX (COLD-) COLD SPRING HARBOR LAB.

XX Greider C, Collins K, Kobayashi R, Yang XH, Hemish UM,
 PI Autexier C;

XX WPI; 1996-309594/31.

XX N-PSDB; AAT30867.

XX Telomerase protein and related DNA, antibodies, transgenic cells, etc. -
 PT for diagnosis and treatment of cancer and infection by eukaryotic
 PT microbes, also new telomerase inhibitors.

XX Claim 10; Fig 2; 56pp; English.

XX AAR96038 and AAR96039 represent Tetrahymena 80 kD and 95 kD proteins (p80
 CC and p95), respectively. These proteins are components of telomerase. The
 CC proteins act, when coupled to RNA, to add telomeric repeats (of the
 CC sequence TTGGGG) to stabilise chromosomes. The RNA component provides the
 CC template for the telomere repeat synthesis. Antibodies against these
 CC sequences, can be used as immunoassay reagents for the detection of the
 CC proteins. The antibodies can also be used to identify immortalised cells,
 CC or predispotion to immortalisation, particularly cancer, or to diagnose
 CC a disease caused by a eukaryotic microbe. Inhibitors of these proteins
 CC (and these proteins themselves) can be used for therapy or diagnosis. The
 CC inhibitors can be used to treat infection by fungi and protozoa. As
 CC somatic cells do not generally require telomerase, these inhibitors
 CC should have little or no toxicity to the host. The DNA encoding these
 CC sequences are used to produce the recombinant protein, or to isolate
 CC similar genes from other organisms, while transformed cells can be used
 CC in gene therapy

XX Sequence 719 AA;

Query Match 6.5%; Score 180.5; DB 2; Length 719;

Best Local Similarity 20.7%; Pred. No. 9.5e-07; Indels 149; Gaps 29;

Matches 115; Conservative 100; Mismatches 191;

QY 102 CSDISTKQAFKAVSEVCIPTHLFTPIQPKDKESMCGMGWALKAIDWNEKG 161
 DB 193 CTESQRKTMFRYLS-----VTNKKMDQTKKKRKENLITKL--QAIKSEDSKRETD 245
 QY 162 M-----ALALATK--YKORNGMSHNDLRLSHLK-PSEGLAVTKYTKGWKEVH 210
 DB 246 INNVEDAIKALPRAWKTIARQNMK-----KMKAPKIPNSTLESKITL-----FK 293
 QY 211 ELYEKALSVETKLLKYLEAVEKYRTKQDELEVIH-----LIEHRLVREHLLT 260
 DB 294 DLIKCHISEPKEARYKILG--KKYPKTEBYKAAFQGSASAPFNPBLAGKMKIEISKT 351
 QY 261 --NHLKSK---EYKALI--QEMPTALLRNIGKNTANSVLEPNSV--SLYCEKCN 310
 DB 352 WENBELSAKNTAEVNDNLISNQLPYMMLRN-----SNLIKAGVSDTHSIVINKICE 406
 QY 311 EKLKKARIHPHILLALETY-----KTGHGLRGKL-----KWRPDE 347

Db 407 PKAVENSGMEPLQFPFSAIEAVNEAVTKGFPKAKKEKNMLKGQIEAVKEVVEKTDDEKKDM 466
 Qy 348 EILKALDAAPFKTKTPTKTPGKRF-----LAV-----DVSASMNQR 384
 Db 467 ELEETEEGERF--VKVNEGIGKQYINSIELATIKIAVNKNLDEIKGHTAITSVSGSMSTS 523
 Qy 385 VLGSILNASTVAAM-----CWVVRTEKDSYVV--AFSDENVPQPVTTDM-----428
 Db 524 MSGGAKKYGVSVRTLECALVIGLNVKQRCESFYIFSSPSQCNKCYLEVDLPGDELRLP 583
 Qy 429 TLQCVLMAHQIPAGGTDCLPMI--NAQKTNPADVPFYFTDNETAG-----GVHP 479
 Db 584 SMQGLDQEKGLT-GGGTDPFYECIDEWT-KXKTHVDNI VIIISDMIAAGVSDINRGSSI 641
 Qy 480 AIALREYRKXMDIPAKLIVGQMTSG--FTIADP-DDRGMDMGCPDTGAL-----527
 Db 642 VNSIKTKKDEVENPIKIPAVDLBGYKCLNLDGFENNNTKIKYMGSDSILKPTISAKQG 701
 Qy 528 ----DVIRNFTLDMV 538
 Db 702 ANWVEVKNPFLQKI 716
 RESULT 13
 ID ADQ66766 standard; protein; 712 AA.
 AC ADQ66766;
 DT 07-OCT-2004 (first entry)
 DE Novel human protein sequence #1739.
 XX
 KM osteopathic; neuroprotective; nootropic; antiparkinsonian; cytostatic;
 KM gene therapy; diagnostic marker; morbid state; osteoporosis;
 KM neurological disease; Alzheimer's disease; Parkinson's disease; dementia;
 KM cancer.
 XX
 OS Homo sapiens.
 PN EPI440981-A2.
 PD 28-JUL-2004.
 PR 21-JAN-2004; 2004EP-00001196.
 PR 21-JAN-2003; 2003JP-00102206.
 PR 09-MAY-2003; 2003JP-00131392.
 PA (REAG-) RES ASSOC BIOTECHNOLOGY.
 PI Isegai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
 PI Yamamoto J, Isono Y, Nagai K, Irie R;
 DR WPI; 2004-535376/52.
 DR N-PSDB; ADQ64576.
 PT Novel 2495 cDNA, useful for treating osteoporosis, neurological diseases,
 PT Alzheimer's diseases, Parkinson's diseases, dementia and various cancers.
 PS Claim 1; SEQ ID NO 3927; 2449pp; English.
 XX The invention relates to 2495 novel polynucleotides (I) and their encoded
 CC polypeptides, sequences hybridizing to these nucleotides, sequences
 CC encoding partial polypeptides and sequences having 70% or 90% identity to
 CC the nucleotide and protein sequences. The nucleotides and polypeptides
 CC are useful as diagnostic markers or therapeutic target for the diseases
 CC or morbid states. They are also useful for treating osteoporosis,
 CC neurological diseases, Alzheimer's diseases, Parkinson's diseases,
 CC dementia and various cancers. This sequence corresponds to a protein
 CC Sequence 712 AA;
 XX
 XX

Query Match 5.1%; Score 143.5; DB 8; Length 712;
 Best Local Similarity 23.7%; Pred. No. 0.0022;
 Matches 82; Conservative 52; Mismatches 115; Indels 97; Gaps 15;
 Qy 46 YIYKEQTLGLENBALIRLIEDRGCEVIOEIKSPGQERTTQEPMLFALACSCSDI 105
 Db 20 YHYKEQRLALA-LDEYVRL-NDAYKESGSHSLFGSGSSSTYDPIILK-----AEI 70
 Qy 106 STKQAAFKAVS-EVCHIPHTL-----FPFIQPKDLKESMGCGMG-----145
 Db 71 STIRLRYKELKRLSQKQELLYKEGFETLQ--QIDKMSGGSGEYELSEAKAII TEL 127
 Qy 146 RALRKAIDWYNEKGWALALAVTKYK---QNGNSHKDL-----182
 Db 128 KSIIRKAISSGEKKQDLMQSLAKLQERPHLDQNIIGSEPLRQSPVNSHLCISQTL DAG 187
 Qy 183 -----LRLSHLKPSEGLAL-VTYITGMEKVEHLYEKA 217
 Db 188 SQTSISGDIGVRSRSLAEKVRSLQYEAKRSMANKIKELSKDSEAWPGALDIEKEL 247
 Qy 218 LSV-ETREKLIKYLEAVEKVKRTKQELVHILIEHRLVREHL-----LTNHLKSKE 267
 Db 248 MLINKEBELKELQPYTPQKRTQDEBLRLR-AERQRLSEELSYRGTPSRALERLRLER 306
 Qy 268 VPRALQEMPLETALL-----RNLGKMTANSV-LEPGNSEVSLVCEK 307
 Db 307 RRKEILQKLEETTKLTLYLHSLQKLSASSTLSMSGSSGLSLASSR 352
 RESULT 14
 ID ADC30964 standard; protein; 1094 AA.
 AC ADC30964;
 DT 18-DEC-2003 (first entry)
 DE Human novel polypeptide sequence, SEQ ID NO:1046.
 XX
 KM Human; diagnostic; drug screening; forensics; gene mapping;
 KM biodiversity assessment; Parkinson's disease; Alzheimer's disease;
 KM neurodegenerative diseases; anaemia; platelet disorder; wound; burns;
 KM ulcers; osteoporosis; autoimmune disease; cancer;
 KM molecular weight marker; food supplement; antiparkinsonian; nootropic;
 KM neuroprotective; anti-nausea; anticogulant; thrombolytic; vulnerytic;
 KM anticancer; osteopathic; immunosuppressive; antiinflammatory; cytostatic;
 KM gene therapy.
 XX
 OS Homo sapiens.
 PN W02003029271-A2.
 PD 10-APR-2003.
 PR 24-SBP-2002; 2002WO-US030474.
 PR 24-SBP-2001; 2001US-0324631P.
 PA (HYSE-) HYSEQ INC.
 PI Tang TY, Zhang J, Ren F, Xue AJ, Zhao QA, Wang J, Wehrman T;
 PI Zhou P, Ghosh M, Wang D, Ma Y, Asundi V, Wang Z, Weng G;
 PI Haley-Vicence D, Drmanac RT;
 DR WPI; 2003-371981/35.
 DR N-PSDB; ADC29993.
 PT New polynucleotide and polypeptide useful for diagnosing, preventing or
 PT treating conditions such as neurodegenerative diseases, anemias, platelet
 PT disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or
 PT cancer.
 XX
 XX

XX Claim 20; SEQ ID NO 1046; 1185bp; English.

XX The invention relates to 971 novel human cDNA sequences (ADC39919-
CC ADC30889) and the polypeptides they encode (ADC30890-ADC31860). The
CC invention also relates to nucleic acid sequences over 99% identical with
CC the novel human cDNAs. The invention additionally encompasses expression
CC vectors and host cells comprising a nucleic acid of the invention; the
CC recombinant production of a polypeptide of the invention; an antibody
CC against a polypeptide of the invention; a method of detecting
CC polynucleotides or polypeptides of the invention; and methods of
CC identifying a compound which binds to a polypeptide of the invention. The
CC invention further discloses methods of preventing, treating or
CC ameliorating a medical condition; kits comprising polynucleotide probes
CC and/or monoclonal antibodies for carrying out the methods of the
CC invention; methods for the identification of compounds that modulate the
CC expression or activity of the polynucleotide and/or polypeptide; and 767
CC contig sequences corresponding to the cDNA sequences of the invention
CC (ADC31861-ADC32627) and the polypeptides encoded by the contigs (ADC32628
CC -ADC33941). The nucleic acids and polypeptides of the invention are
CC useful in diagnostics, drug screening, forensics, gene mapping, in the
CC identification of mutations responsible for genetic disorders or other
CC data, for assessing biodiversity, and in producing many other types of
CC drugs and products dependent on DNA and amino acid sequences. They are
CC also used for treating diseases such as Parkinson's disease, Alzheimer's
CC disease and other neurodegenerative diseases, anaemia, platelet
CC disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or
CC cancer. The nucleic acids may also be used as hybridisation probes or
CC primers, and in the recombinant production of a protein. The polypeptides
CC are also useful in generating antibodies, as molecular weight markers,
CC and as food supplements. The present sequence represents a specifically
CC claimed human polypeptide sequence of the invention. Note: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 1094 AA;

Query Match 5.1%; Score 143.5; DB 7; Length 1094;
Best Local Similarity 23.7%; Pred. No. 0.0043;
Matches 82; Conservative 52; Mismatches 115; Indels 97; Gaps 15;

QY 46 YVKEKQKGLNNAALIRLIEDRGCEVIOEIKSFQSGERTTKQEBMFLPALMICSCSDI 105
DB 20 YVKEGRRLA-LDEVYRL-NDAYKKESSSHSTSLFSGSSSTKYDPDIK-----AEI 70
QY 106 STKOAFKAVS-EVCRIPTHL-----FTFIQKDKLKSMTKGMWG----- 145
DB 71 STTRLRVKKLKKRELQSMQKELLYKEGCFETLQ---QIDKMSGGSGCYELSEKALITEL 127
QY 146 RALRKAIADWYNEKGMALALAVTKYK---QNGNSHDL----- 182
DB 128 KSIKRAISSGEKQKQMLQSLAQERPHLDQNGISEPDLRCSPVNSHLCLSRQTLDA 187
QY 183 -----LRLSHKPSSEGLAI-VTKYITKMKVEHYELYKKA 217
DB 188 SQTSGISGDIQVRSNIAEKVRLSLQYBEAKRSMANIKELSLQDSBAMFGALDIKEKA 247
QY 218 LSV-ETREKLLKYEAVERKVKTKQDELIVHILIEHRLVREHL-----LTNHLKSKE 267
DB 248 MLINKESELKELQFVTPQKTKQDEBELERL-AERQRLBELLSVVRGTPSALAERLER 306
QY 268 VWRKLLQEMPLETALL-----RNLGKRYTANSV-LEPGNSEVSLCEK 307
DB 307 RRRELLQKLEETTKLTTYLHSQLKSLASASTLSMSSGSLASASR 352

RESULT 15

ADQ17289 ID ADQ17289 standard; protein; 1937 AA.

XX AC ADQ17289;

XX XX 26-AUG-2004 (first entry)

XX Human soft tissue sarcoma-upregulated protein - SEQ ID 106.

XX soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human.

XX Homo sapiens.

XX MO2004048938-A2.

XX 10-JUN-2004.

XX 26-NOV-2003; 2003WO-US038193.

XX 26-NOV-2002; 2002US-0429739P.

XX (PROT-) PROTEIN DESIGN LABS INC.

XX Aziz N, Ginsburg WM, Zlotnick A;

XX WPI; 2004-441208/41.

XX Early detection of soft tissue sarcoma comprises determining expression
XX of a gene in a first soft tissue sample and a normal soft tissue sample
XX and comparing the gene expression, also useful in treating soft tissue
XX sarcoma.

XX Example 2; SEQ ID NO 106; 210bp; English.

XX The invention relates to a novel method for detecting soft tissue sarcoma
XX which comprises obtaining a first soft tissue sample from an individual
XX and a normal soft tissue sample from the same or different individual,
XX determining the expression of a gene in both samples and comparing the
XX expression of the gene in both soft tissue samples, where a higher level
XX of protein expression in the first soft tissue sample indicates the
XX presence of soft tissue sarcoma. The method of the invention has
XX cytostatic applications and may be useful for detecting soft tissue
XX sarcoma, possibly via gene therapy or vaccine production. The nucleic
XX acid sequences may be useful in diagnostic and screening applications.
XX The current sequence is that of a human soft tissue sarcoma-upregulated
XX protein of the invention. The current sequence is not shown within the
XX specification per se but was submitted in CD format by the inventor.

XX Sequence 1937 AA;

Query Match 4.7%; Score 130.5; DB 8; Length 1937;
Best Local Similarity 20.0%; Pred. No. 0.16;
Matches 101; Conservative 72; Mismatches 168; Indels 165; Gaps 18;

QY 1 MEESVNOQGPLNEKO-----IANSQDGVVMQVTDNRLRFLCGSEGGTY 47
DB 1255 LEDQVSELTKEEBQORLINDITQAPARLQTAGVYSQIDKDALVSLSSKQASTQ 1314
QY 48 IKKQKGLN-----AEALIRLEDGR-GCEVIOEIKSFQSGERTTKQEBMFLPALMICSC 102
DB 1315 IBEHQLEEFERKARALALAHQSSHDCDLRBEQYEEBQKALQ----- 1361
QY 103 STIKOAFKAVSEVCRIPTHLP-PIQPKDKL-----SMKCG 142
DB 1362 -----RALSKANSEVAQWRITYETDALQRTTELEBAKKQLAQRLQBAEHEVAANAKKA 1415
QY 143 MNGRALRKAIADWYNEKGMAL-----ALAVTKYKORN-----GWSHK----- 180
DB 1416 -----SLEKTKQRLQNEVEDLMDVERSNACALDKQKNPDKVLSWKQKTEFTQAELE 1471
QY 181 -----DLRLSHL-----KPSSEGLAIVTKYITKMKVEHYELYK 214
DB 1472 ASQKESRSLSLEFKKQVYVESLDQLFTLRBNKKLQOEISDLFTQIABGGKQIHELK 1531
QY 215 EKALSVTEKLLKYEAVERKVKTKQDELIVHILIEHRLVREHLTNHLKSKEVWQALLQ 274
DB 1532 IKK-QVEQKRC-----EIOALAEAEASLEHEBGKILIRIQLELNVKSEVDRKIAEK 1582
QY 275 EMPITLALNIGM--TANSVLEPG-----NSEVSLVCEK 307

Db 1583 DEIDQJKNRTRVETMSTLDAIRSRNDALRVKKKMGEDLNEMEIQLNHANRLAAS 1642
QY 308 LCN---EKLIKARIRHPHILIALETYKTGHGUGKIKMRPDEIILK---ALDAAPYK 359
Db 1643 LRNYRNTOGILKETQLH-----LDDALRGQEDLKEQLAIVERRANLIQAEIEE 1690
QY 360 TPKTVEPTGKRFLAVDVASAMNORV 385
Db 1691 LWATTLEOTERSRKIAEQELLDASERV 1716

Search completed: January 13, 2006, 11:09:15
Job time : 82 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: January 13, 2006, 11:07:29 ; Search time 26 Seconds
(without alignments)
1710.751 Million cell updates/sec

Title: US-10-615-515-6

Perfect score: 2787
Sequence: 1 MEEVNMQPLNEKQIANSQ.....MCGFDGALDVIRNFTLMT 538

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: Issued Patents PA:*

- 1: /cgn2_6/ptodata/1/1aa/5-COMB.pep:*
- 2: /cgn2_6/ptodata/1/1aa/6-COMB.pep:*
- 3: /cgn2_6/ptodata/1/1aa/H-COMB.pep:*
- 4: /cgn2_6/ptodata/1/1aa/PCITUS-COMB.pep:*
- 5: /cgn2_6/ptodata/1/1aa/RB-COMB.pep:*
- 6: /cgn2_6/ptodata/1/1aa/backfilest1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2784	99.9	542	2	US-09-949-016-10805
2	180.5	6.5	699	2	US-08-851-843A-52
3	180.5	6.5	699	2	US-08-851-843A-52
4	180.5	6.5	699	2	US-08-854-050-52
5	180.5	6.5	699	2	US-08-854-050-52
6	180.5	6.5	699	2	US-09-402-181B-188
7	180.5	6.5	699	2	US-09-402-181B-188
8	180.5	6.5	699	2	US-09-766-253-52
9	180.5	6.5	699	2	US-10-054-295-52
10	180.5	6.5	699	2	US-09-438-486A-52
11	180.5	6.5	719	2	US-08-851-843A-7
12	180.5	6.5	719	2	US-08-974-549A-219
13	180.5	6.5	719	2	US-08-854-050-7
14	180.5	6.5	719	2	US-09-430-323-7
15	180.5	6.5	719	2	US-09-402-181B-219
16	180.5	6.5	719	2	US-09-721-456-219
17	180.5	6.5	719	2	US-09-766-253-7
18	180.5	6.5	719	2	US-10-054-295-7
19	180.5	6.5	719	2	US-09-438-486A-7
20	130.5	4.7	1937	2	US-09-538-092-918
21	123	4.4	23	2	US-08-475-955-48
22	123	4.4	23	2	US-07-867-819D-48
23	118	4.2	713	1	US-08-484-933B-2
24	118	4.2	713	1	US-08-484-158B-2
25	118	4.2	713	1	US-08-484-596A-2
26	118	4.2	713	1	US-08-480-150A-2
27	118	4.2	713	2	US-08-458-731-2

28	118	4.2	713	2	US-08-149-223A-2	Sequence 2, Appl1
29	116	4.2	21	2	US-08-716-249-11	Sequence 11, Appl1
30	116	4.2	22	2	US-08-475-955-55	Sequence 55, Appl1
31	116	4.2	22	2	US-07-867-819D-55	Sequence 55, Appl1
32	115.5	4.1	550	2	US-10-104-047-3495	Sequence 3495, Ap
33	113.5	4.1	1802	2	US-09-949-016-11073	Sequence 11073, A
34	113	4.1	1939	2	US-09-538-092-915	Sequence 915, App
35	113	4.1	1939	2	US-09-949-016-11104	Sequence 11104, A
36	110.5	4.0	709	2	US-09-328-352-5172	Sequence 5172, Ap
37	110.5	4.0	1979	2	US-09-949-016-5468	Sequence 5468, Ap
38	110.5	4.0	2047	2	US-09-949-016-7404	Sequence 7404, Ap
39	110.5	4.0	2186	2	US-09-949-016-10828	Sequence 10828, A
40	110.5	4.0	2349	2	US-09-538-092-914	Sequence 914, App
41	110	3.9	952	2	US-09-620-405B-475	Sequence 475, App
42	110	3.9	1002	2	US-09-604-287A-475	Sequence 475, App
43	110	3.9	1002	2	US-09-834-759-475	Sequence 475, App
44	110	3.9	1002	2	US-09-590-751A-475	Sequence 475, App
45	110	3.9	1002	2	US-09-590-751A-475	Sequence 475, App

ALIGNMENTS

```

RESULT 1
US-09-949-016-10805
; Sequence 10805, Application US/09949016
; Patent No. 6812319
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001107
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10805
; LENGTH: 542
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10805
Query Match          99.8%; Score 2784; DB 2; Length 542;
Best Local Similarity 99.8%; Pred. No. 2.3e-258;
Matches 537; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
1 MEEVNMQPLNEKQIANSQDGYVQVTDNMLHREFLCGSEGGTYIYKEQKLGLENADA 60
5 MEEVNMQPLNEKQIANSQDGYVQVTDNMLHREFLCGSEGGTYIYKEQKLGLENADA 64
61 LIRLIEDGGCGVIOEIKSFSGEGRTTKOEPMLPALITSQCSQSDISTKQAAKVAEVR 120
LIRLIEDGGCGVIOEIKSFSGEGRTTKOEPMLPALITSQCSQSDISTKQAAKVAEVR 124
65 LIRLIEDGGCGVIOEIKSFSGEGRTTKOEPMLPALITSQCSQSDISTKQAAKVAEVR 124
121 IPTHLPTRFQPKDDKESKCGMGRALRKALADVNEKGMALALAVTRYKORNSMK 180
125 IPTHLPTRFQPKDDKESKCGMGRALRKALADVNEKGMALALAVTRYKORNSMK 184
181 DLIRLSHLKPSSEGLAVTYTKGWEVHELYKEKALSVETEKLLKYLAIVEKYRTYD 240
185 DLIRLSHLKPSSEGLAVTYTKGWEVHELYKEKALSVETEKLLKYLAIVEKYRTYD 244
241 ELEVIHLIEHRLVREHLLTNHLKSEVKKALLQEMPTALLRNIGKATNSVLEPGENSE 300
245 ELEVIHLIEHRLVREHLLTNHLKSEVKKALLQEMPTALLRNIGKATNSVLEPGENSE 304
301 VSLVCKKCNELKKARLHPHILLALFTYTKGHLRGKLMWRPDEITLKALDAAFYKT 360

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Db      305 VSLVCEGLCHNEKLIKQKRIHPHILILALETYKTHGRLGKLPDDEIILKALDAAYTK 364
Qy      361 FKVEPTGKPEFLADVVSASHNQRVLGSIINASTVAAAMCVVTRTEKDSYVAFSDEMY 420
Db      365 FKVEPTGKPEFLADVVSASHNQRVLGSIINASTVAAAMCVVTRTEKDSYVAFSDEMY 424
Qy      421 PCPTTMTLOQVLMASQIPAGGTDGSLPMIWAOKTNPADVIVFTDNETFAGVHPA 480
Db      425 PCPTTMTLOQVLMASQIPAGGTDGSLPMIWAOKTNPADVIVFTDNETFAGVHPA 484
Qy      481 IALREYRKMDIPAKLIYCGTNSGFTIADDDRGMLDMCGFDGALDVIRNFTLDMI 538
Db      485 IALREYRKMDIPAKLIYCGTNSGFTIADDDRGMLDMCGFDGALDVIRNFTLDMI 542

RESULT 2
US-08-851-843A-52
; Sequence 52, Application US/08851843A
; Patent No. 6093809
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin H.
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: No. 6093809e1 Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/851,843A
; FILING DATE: 06-MAY-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 699 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; JUS-08-851-843A-52

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Query Match      6.5%; Score 180.5; DB 2; Length 699;
Best Local Similarity 20.7%; Pred. No. 3,6e-08;
Matches 115; Conservative 100; Mismatches 191; Indels 149; Gaps 29;

Qy      102 CSDISTKQAFKAVSEVCRIPHTLFTIOPKDLKESMCKGMGRALKA1ADWYNEKG 161
      175 CTSQRKKTFRYLS-----VTNKQKWDQTKKRXKENTLTKL--QAIKESDSKRETD 227
Qy      162 M-----ALALAATK--YKQKNGSHKDLKLSHK-PSSEGLAVTYKITGMEVH 210
      228 IMMVEDAIKILKAVMKKIAKQNAK-----KHKAKKIPNSTLESKYL-----FK 275
Qy      211 ELYEKALSVETETLKYLEAVEKVKRTKDELYIH-----LIBHRLVREHLLT 260
      276 DLTKFCHISEPKERVYKILG--KPYKTEEEYKAAFGDSASAPNPFLACKMKIESTK 333
Qy      261 --NHLKSK---EYWKAL--QEMPLTALRLNGKMTANSVLBFGNSEV--SLVCEKLCN 310
      334 WENELSAKNTAEVMDLISNQLPYVAMLRNL-----SNILKAGVSDTTHSYVINKICE 388
Qy      311 EKLKARIRHPHILILALETY-----KTGHLGKLT-----KMRPDE 347
      389 PKAVENSKMFPLOFFSAIEAVNEAVTKGFRKQKQENNLKGQIEAVKEVEKTDDEKKDM 448
Qy      348 EILKALDAAFYKTFKTEPTGKPEFL-----LAV-----DVASAMNOR 384
      449 ELETGEBGEF--VKNEGIGKQYINSIELAIKIAVNKNLDEIKGHTAIRSDVSGSMSTS 505
Qy      385 VLGSILNASTVAAAM-----CNVYTRTEKDSYV--AFSDEMYPCPVTTDM----- 428
      506 MSGGAKKYGSVRCLECALVIGLAVKQRCESKSPYRSPSSQCNKCYLEVDLPGDELRLP 565
Qy      429 TLQOVLMASQIPAGGTDGSLPMI--WAOKTNPADVIVFTDNETFAG-----GVHP 479
      566 SMOGLQEKGLT-GGGDPEPEECIDEWT-KKKTHVDIVILSDMMIAEGVSDINVRSSI 623
Qy      480 AILREYRKMDIPAKLIYCGTNSG--FTIADP-DDRGMLDMCGFDGAL----- 527
      624 VNSIKKIKDEVNRIKIFAVDLBGYKCLALGDEFENNNYIKIFGMSDILKFTSAKQG 683
Db      528 ----DVIRNFTLDMI 538
      684 ANNVEVIKNFALOKI 698

RESULT 3
US-08-974-549A-188
; Sequence 188, Application US/08974549A
; Patent No. 6166178
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin H.
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

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1      APPLICATION NUMBER: US/08/974,549A
2      FILING DATE: 19-NOV-1997
3      CLASSIFICATION: 536
4      PRIOR APPLICATION DATA:
5      APPLICATION NUMBER: US 08/724,643
6      FILING DATE: 01-OCT-1996
7      PRIOR APPLICATION DATA:
8      APPLICATION NUMBER: US 08/844,419
9      FILING DATE: 18-APR-1997
10     PRIOR APPLICATION DATA:
11     APPLICATION NUMBER: US 08/846,017
12     FILING DATE: 25-APR-1997
13     PRIOR APPLICATION DATA:
14     APPLICATION NUMBER: US 08/851,843
15     FILING DATE: 06-MAY-1997
16     PRIOR APPLICATION DATA:
17     APPLICATION NUMBER: US 08/854,050
18     FILING DATE: 09-MAY-1997
19     PRIOR APPLICATION DATA:
20     APPLICATION NUMBER: US 08/911,312
21     FILING DATE: 14-AUG-1997
22     PRIOR APPLICATION DATA:
23     APPLICATION NUMBER: US 08/912,951
24     FILING DATE: 14-AUG-1997
25     PRIOR APPLICATION DATA:
26     APPLICATION NUMBER: US 08/915,503
27     FILING DATE: 14-AUG-1997
28     PRIOR APPLICATION DATA:
29     APPLICATION NUMBER: WO PCT/US97/17618
30     FILING DATE: 01-OCT-1997
31     PRIOR APPLICATION DATA:
32     APPLICATION NUMBER: WO PCT/US97/17885
33     FILING DATE: 01-OCT-1997
34     ATTORNEY/AGENT INFORMATION:
35     NAME: Apple, Randolph Ted
36     REGISTRATION NUMBER: 36,429
37     REFERENCE/DOCKET NUMBER: 015389-002610US
38     TELECOMMUNICATION INFORMATION:
39     TELEPHONE: (415) 576-0200
40     TELEFAX: (415) 576-0300
41     INFORMATION FOR SEQ ID NO: 188:
42     SEQUENCE CHARACTERISTICS:
43     LENGTH: 699 amino acids
44     TYPE: amino acid
45     STRANDEDNESS:
46     TOPOLOGY: linear
47     MOLECULE TYPE: peptide
48     US-08-974-549A-188

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[illegible]

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QY      348 ELIKALDAFYPTKPTVEPTGRFL-----LAV-----DIVSANNOR 384
Db      449 ELKQTEGEF---VKNNEGIKQYINSLIELAKIANKNDEIKGHTAIPSDVSGSWSTS 505

QY      385 VIGSIINASTVAAM-----CQVVTREKOSIVV--AASDEKVPQPVTTM----- 428
Db      506 MSGGAKKYSVATTCLEALVLGLMKORCEKSPFISSPSSQCNKCYLEVLDPGBELRP 565

QY      429 TLQOVLVAMASQIPAGSTDCSLPMI--MAQKNTPTADVFIPTDNDETFAG-----GVHP 479
Db      566 SMLKTLQEGKGL--GGSTDPPEYCIDEMI--KKKTHVDNIVLISDPMIAEGVSDINVRSSSI 623

QY      480 AIALREYRKMDI PAKLVICGNTSNG--FTIADP--DREGMLDMCGFPTGL----- 527
Db      624 VNSIKKYKQEVNPNKIFAVLDLEGYKCLNLGDEFENNENYIKIFGMSDSILKFI SAKQGG 683

QY      528 ----DVIRNFTLMDI 538
Db      684 ANNVEVITKFNPALOKI 698

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RESULT 4
US-08-854-050-52
Sequence 52, Application US/08854050
Patent No. 6261836
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Hartley, Calvin
APPLICANT: Andrew, William H.
TITLE OF INVENTION: No. 6261836el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-MAY-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200

```

? TELEFAX: (415) 576-0300
? INFORMATION FOR SEQ ID NO: 52
? SEQUENCE CHARACTERISTICS:
? LENGTH: 699 amino acids
? TYPE: amino acid
? STRANDEDNESS:
? TOPOLOGY: linear
? MOLECULE TYPE: peptide
? OS-854-050-52

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Query Match	6.5%;	Score 180.5;	DB 2;	Length 699;
Best Local Similarity	20.7%;	Pred. No. 3.6e-08;		
Matches 115;	Conservative 100;	Mismatches 191;	Indels 149;	Gaps 29;

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Qy 102 GSPISRTKOAFAKXAVSEVCEI PTHLETFLOPKDLESKCCMBWRALAIADVYNEKG 161
Db 175 CTESQKRTKMFRLS-----VTNRQKMDOTKKGRKENLTLTL--QALKESDSSKRTGD 227
Qy 162 M-----ALALAVTK--YKORNGSMKDLRLSHLK-PSSEGLAVTKYITKWKVEVH 210
Db 228 IMNVEDAIKALKKPAVMKKIAKQNAK-----XHMCAPKIPNSTLESKYLT-----FK 275
Qy 211 ELYEKALSVTEKLLKLYLEAVEKVKRTDELEVH-----LIEHRLVREHLT 260
Db 276 DLTKFCHISEPKERYVYKLG--KKYPKTEEYKAFAFGSASAPNPBLAGKRMKEISKT 333
Qy 261 --NHLKSK-----EVMYALN--OBMPLTALRYLGQWTANSVLEPQNSEV--SLVCEKLN 310
Db 334 WEHELKAKGTAEVNMNLISNSQLPYMMALRNL-----SNLIKAGVDTHTSHIYINKICE 368
Qy 311 EKLKARAIHPHILIALETY-----KTGHGLRGKL-----KMRPDE 347
Db 389 PKAVENSKMPPLQFSAIEAVNEAVTKGPKAKGRZNNMLKQGLEAVEKVEKTEBEEKDM 448
Qy 348 EILKALDAAPYTKFKVEPTGKRF--LAV-----DVASANKOR 384
Db 449 ELKOTEGEFP--VKNEBIGKQYINSLELAKIAVNNKLNDEIKGHTAIFSDVSGSMSTS 505
Qy 385 VLGSILNASTVAANM-----CMVYTRTEKDSYVV--AFSDENVPYCPTVDM----- 428
Db 506 MSGGAKKYGVSRTCELCALVGLAMKORCEKSFITFSSPSQCNKCYLEVDLFGDELRP 555
Qy 429 TLQOVLWAMSQIPAGSGTDSLPMI--WAKOXTNPADVEIVFTDNETPAG-----GVHP 479
Db 566 SMQKTLQEKKGL--GGGTDPRPYECIDBWT--KNKTHVDNVLISDMMIALGVSADINVRSSI 623
Qy 480 AIALREYRKMDIPAKYLIVCGMTSNG--FTIADP--DDBGMLDMGCFDTGAL----- 527
Db 624 VNSIKKQKEVENENIKIIPAVDLEGYKCLINLQDEBENNENYIKIFQMSDSILKFIASQOG 683
Qy 528 ----DVIRNFTLMI 538
Db 684 ANNVEVYKNFALOKI 698

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RESULT 5
US-09-430-323-52
! Sequence 52, Application US/09430323

GENERAL INFORMATION:
APPLICANT: Cecch, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morrin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: No. 630967e1 Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco

STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/430,323
FILING DATE: 29-Oct-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA: US 06/0574,070

Query Match	6.5%;	Score 180.5;	DB 2;	Length 699;
Best Local Similarity	20.7%;	Pred. No. 3.6e-08;		
Matches 115;	Conservative 100;	Mismatches 151;	Indels 149;	Gaps 29;

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0Y 102 CSDISTOQAAPKAVSEWCRIPTHLPTFIQFKDILKESMKCSMGRLAKAIADMYNKEGG 161
Db 175 CTESQORKKMERVYL-----VTNQKMDQOTKKKRENILTYL--QALISEDSKSRLEGG 227
0Y 162 M-----ALALAVTK--YKORGNHSHKULLRLSHLK-PSEGLALVTKIYTGMEVH 210
Db 228 IMANVEDAIKALKPAMVKKIARQAMK-----KHKAPKIPNSTLESKYLT-----FK 275
0Y 211 ELYEKALSVTEGLKYLEAVEKVKRTOLEVIH-----LIEHRILVREHLLT 260
Db 276 DLIRFCHISEPKEVYKILG--KKYPTKEEYKAPFGDSASAPNPNBELAGRMKIEISK 333
0Y 261 --NHLKSK---EYWKOLL--QEMPLTALLNLGOMTANSVLBPNGNSEV--SLVCEKLCN 310
Db 334 WENELISAAGNTAEAWNDLISNOPLPYAMALNLL-----SNLKAGVSDTTHSYINKCE 388
0Y 311 EKLTKKARIHPHILIALETY-----XYGHLGRGL-----KWRPDE 347
Db 389 PKAVENSGMPLQOPFSAIEAVNEAVTGFKAKKRENNLKKQIEAVKEVEKTBDEKKDM 448
0Y 348 EILKALDPAFYKTEKTEVEPTGRFL--LAV-----DVSAQNOR 384
Db 449 ELBQTESEEF---VKANEGIGKQYINSIELAKIAYVNNGLDEIKGHTAIPSDVGSGMSTS 505
0Y 385 VLGSILNASTVAAAM-----CMVVTREKDSYVV--APSDENVPCPVTTDM----- 428
Db 506 MSGGAKKYGVSVRTGLECALVLGLMWKORCEKSGSFYIFSSPSSQCNKCYLAEVDLPDELDLP 565
0Y 429 TLQOVLNAMSQIPAGGIDCSLPMI--MAQKTNPADVPYIVTDMETPFG-----GHP 479

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Db 566 SMOQLQKQKX-GGTDFPEYCEIDEMT-KNKTVDNIVILSDMMIABGYSDINVRGSSI 623
 Qy 480 AIALREYKRDIDPAKLIYCGWTSNG--FTIADP-DDRGMLDMCGFDYCAL----- 527
 Db 624 VNSIKKYDEVNPNIKIPAVDLBGYKCLNLGDEFENNNYIKIPGMSDILKFIKAKQGG 683
 Qy 528 ----DVIRNFTLDMT 538
 Db 684 ANMVEVINKPFLQKI 698

RESULT 6
 US-09-402-181B-188
 Sequence 188, Application US/09402181B
 Patent No. 6610839

GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.
 Langer, Joachim
 Nakamura, Toru
 Chapman, Karen B.
 Morin, Gregg B.
 Harley, Calvin B.
 Andrews, William H.
 TITLE OF INVENTION: Human Telomerase Catalytic Subunit
 NUMBER OF SEQUENCES: 633
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, Eighth Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/402,181B
 FILING DATE: 29-Sep-1997
 CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/724,643
 FILING DATE: 01-OCT-1996
 APPLICATION NUMBER: US 08/844,419
 FILING DATE: 18-APR-1997
 APPLICATION NUMBER: US 08/846,017
 FILING DATE: 25-APR-1997
 APPLICATION NUMBER: US 08/851,843
 FILING DATE: 06-MAY-1997
 APPLICATION NUMBER: US 08/854,050
 FILING DATE: 09-MAY-1997
 APPLICATION NUMBER: US 08/911,312
 FILING DATE: 14-AUG-1997
 APPLICATION NUMBER: US 08/912,951
 FILING DATE: 14-AUG-1997
 APPLICATION NUMBER: US 08/915,503
 FILING DATE: 14-AUG-1997
 APPLICATION NUMBER: WO PCT/US97/17885
 FILING DATE: 01-OCT-1997

ATTORNEY/AGENT INFORMATION:

NAME: Ausenius, Scott L.
 REGISTRATION NUMBER: 42,271
 REFERENCE/DOCKET NUMBER: 015389-002620US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 TELEFAX: (415) 576-0300
 INFORMATION FOR SEQ ID NO: 188:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 699 amino acids
 TYPE: amino acid
 STRANDEDNESS: <Unknown>

TOPOLOGY: linear
 MOLECULE TYPE: peptide
 SEQUENCE DESCRIPTION: SEQ ID NO: 188:
 US-09-402-181B-188

Query Match 6.5%; Score 180.5; DB 2; Length 699;
 Best Local Similarity 20.7%; Pred. No. 3.6e-08;
 Matches 115; Conservative 100; Mismatches 191; Indels 149; Gaps 29;

Qy 102 CSDISTKQAFKAVSEVCRITPHLFTPIQFKDLKESKCGMGRALKALADWNEKGG 161
 Db 175 CTESQKKTWFRYLS-----VTNKKQMDTKKKRENNLTGL--QAIKESDRSKRRTGD 227
 Qy 162 M-----ALALAVTK--YKORNGSHKDLRLSLHLK-PSEGLAIYTKYTKGMKEVH 210
 Db 228 IANVEDAIKALKPAWKRIARQNNMK-----KMMAPKIPNSTLSKTLT-----FK 275
 Qy 211 ELYKEKALSVETEKLLKYLBAVEKVKRTKDELEVH-----LIEHRLVREHLLT 260
 Db 276 DLKCHSEPKERYKYLK--KKYKTBEEYKAFGSASAPFNPBLAGRMKIEISKI 333
 Qy 261 --NHLKSK---EWKALL--QEMPTALLNGLGMTANSVLEPNSGV--SLVCEKLCN 310
 Db 334 WENELSAKNTAFVWDNLISNQLPYMAMRLN-----SNILKAGVSDTHSIVINKICE 388
 Qy 311 EKLKKAIRPHHILIALETY-----KTGHGLRGTL-----KMRPDE 347
 Db 389 PAVVNSKGFPLQFPSSALBAVNEAVTKGFKAKGRNNMLKQIABKVEKTEDEKQDM 448
 Qy 348 BILKALDAFYKTFKVEPTGRFL-----LAV-----DVSASMNQR 384
 Db 449 ELBQTEBGEF--VKNVIGIKQYINSIEIAKIAVKNKLDEIKGHTAIFSVSGSMST 505
 Qy 385 VLGSTLNASVVAAM-----CMVVTREKDSYV--AFSDENVPCPYTDM----- 428
 Db 506 MSGGAKKGVSVTCECALVIGLAWKORCEKSFYIFSSPQCKCYLEVLDPGBELRP 565
 Qy 429 TLQOVLAMSQIPAGTDCSLPMI--WAQKNTTPADVPIVFTDNTETFG-----GVHP 479
 Db 566 SMOQLQKQKX-GGTDFPEYCEIDEMT-KNKTVDNIVILSDMMIABGYSDINVRGSSI 623
 Qy 480 AIALREYKRDIDPAKLIYCGWTSNG--FTIADP-DDRGMLDMCGFDYCAL----- 527
 Db 624 VNSIKKYDEVNPNIKIPAVDLBGYKCLNLGDEFENNNYIKIPGMSDILKFIKAKQGG 683
 Qy 528 ----DVIRNFTLDMT 538
 Db 684 ANMVEVINKPFLQKI 698

RESULT 7
 US-09-721-456-188
 Sequence 188, Application US/09721456
 Patent No. 6617110

GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.
 Langer, Joachim
 Nakamura, Toru
 Chapman, Karen B.
 Morin, Gregg B.
 Harley, Calvin B.
 Andrews, William H.
 TITLE OF INVENTION: Human Telomerase Catalytic Subunit
 NUMBER OF SEQUENCES: 727
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, Eighth Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94111-3834
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk

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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/721,456
FILING DATE: 22-No. 6617110-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0280
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 188:
SEQUENCE CHARACTERISTICS:
LENGTH: 699 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 188:
US-09-721-456-188

Query Match      6.5%; Score 180.5; DB 2; Length 699;
Best Local Similarity 20.7%; Pred. No. 3.6e-08;
Matches 115; Conservative 100; Mismatches 191; Indels 149; Gaps 29;

Cy 102 CSDISTQAFKAVSEVCRIPTLFTPIQPKDLKESKCMGGRALKAIADYNEKG 161
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 175 CTESQRRKTKWFRYS-----VTNKOQMDQTKKKRKENLITL--QAIKESDKSKRETD 227
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Cy 162 M-----ALALAVTK--VKORNGMSHKDLRLSLHK-PSEGLAIYTKYITGMKEVH 210
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 228 IANVEDAIKALKPAMVKIARONAMK-----KMKAPKIPNSTLESKLT-----FK 275
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Cy 211 ELYEKALSVETEKLLKYLAEVKKYKDELEVIH-----LIEEHLVREHLIT 260
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 276 DLIFCHISEKKEVYKILG--KKYKPTSEBYKAFGDSASAPNPBLAGKRMIEISKI 333
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Cy 261 --NHLKSK---EYWKAL--QEMPLTLLNLGKMTANSVLEPQNSEV--SLVCEKLCN 310
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 334 WENELSAKAGTAFAVDNLISNOIPYAMLRNL-----SNIKAGVSPJTHSIYINKICE 388
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Cy 311 EKLKAKARIHGFHILIALEY-----KTHGLRGKL-----KMRPDE 347
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 389 PKAVENSMPLOPPSAIEAVNEAVTKGFKAKKERNMLKGQIEAVKEVEKTEDEKKDM 448
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Cy 348 EILKALDAAFKTEKTVPTGKRFV---LAV-----DVSASMNQR 384
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

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Db 449 ELBQTEGEFF---VKVNEGIGQYINSIELAIKIAVKNKLDIEIKGHTAIFSDVSGSNSTS 505
Cy 385 VLGSILNASTVAAM-----CWVYTRTEKDSYV--AFSDENVPCTPTTDM----- 428
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 506 MSGAKKYGSGVRCLEBALVGLMVKORCEKSFYIFSSSQCNKYILEVDLPBGDLRP 565
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Cy 429 TLQOVLMAWSQIPAGTDCSLPMI--WAQKTNTPADVPIVFTDNETPAG-----GVHP 479
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 566 SMQKLGKEKUL-GGGTDPFYECIDEWT-KNKTGHVDNIVILSDPMIAEGYSDINVRGSSI 623
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Cy 480 AIALREYRKMDIPAKLIYCGMTSNG--FTIADP-DRGMLDMCGPPTGAL----- 527
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 624 VNSIKKTKDEVNPIKXFAVDLEGGKCLNLGDEFNENNYIKLFGMSDSILKFIKSAKGG 683
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Cy 528 -----DVIRNFTLMI 538
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 684 ANMVEYIKNPLQKI 698

RESULT 8
US-09-766-253-52
Sequence 52, Application US/09766253
Patent No. 680880
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
            Lingner, Joachim
            Nakamura, Toru
            Chapman, Karen B.
            Morin, Gregg B.
            Harley, Calvin
            Andrews, William H.
TITLE OF INVENTION: No. 680880e1 Telomerase
NUMBER OF SEQUENCES: 171
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/766,253
FILING DATE: 19-Jan-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/846,017
FILING DATE: 1997-04-25
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002920US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 699 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 52:
US-09-766-253-52

Query Match      6.5%; Score 180.5; DB 2; Length 699;
Best Local Similarity 20.7%; Pred. No. 3.6e-08;

```

Matches 115; Conservative 100; Mismatches 191; Indels 149; Gaps 29;

QY 102 CSDISTQAPFAVEVCRIPHTLFTFIOFKDLKESKCGMGRALAKAIADWTNEKG 161
 DB 175 CTESORCKTMFRYLS-----VTNKQKMDQTKKREKENTLTCL--QAIKESBKSKRETFGD 227
 QY 162 M-----ALALAVTK--YKQRNGMSHKDLRLSHLK-PSSEGLAIVTKYITKGMKEVH 210
 DB 228 IMNVEDAIKALKPAAWKIARQNMK-----KHMKAIPKIPNSTLSKYLT-----FK 275
 QY 211 ELYEKALSVETEKLLKYLEAVEKVKRTKDELEVH-----LIEHRLVHEHLLT 260
 DB 276 DLIFCHISEPERKYKILG--KKYPTKEEYKAFGDSASAPFNPBLAGKMKIEISKI 333
 QY 261 --NHLKSK-----EYWKALL--QEMPLTALLRLGKMTANSVLEPNSSEV--SLVCEKLCN 310
 DB 334 WENELSAKGNATAEVNDNLISNQLPYMMLRNL-----SNLKAGVSDTTHSIVINKICE 388
 QY 311 EKLKKAIRHPHILALETY-----KTGHGIRGL-----KWRPDE 347
 DB 389 PRAVENSIOFPLQFSAIEAVNEAVTKGFKAKKRENNMLKQDIEAVKEVEKTDDEKKDM 448
 QY 348 EILKALDAFYKTFVTEPTGRPL-----LAV-----DVSASMNOR 384
 DB 449 ELEQTEBEF--VKVNEGIGKQYINSIELAIKIAVNNKLDRIKHTAIFSDVSGSMSTS 505
 QY 385 VLGSILNASTVAAAM-----CMVTRTEKDSYVV--AFSDENVPCTVTDM-----428
 DB 506 MSGGAKKYGVSATCECALVIGLAWKORCKESSFYIFSSPSSQCKCYLEVLDLPDGLR 565
 QY 429 TLQOVLAMMSQIPAGTDCSLPMI--MAOKTTPADVTFVFDNTEFTAG-----GVHP 479
 DB 566 SMQKLOEGKGL--GGTDFPYECIDEMT--KNKTHVDNVIYLSDDMIABEYSDINVRGSSI 623
 QY 480 AIALREYRKMDIPAKLIVCGWTSNG--FTIADP--DDRGMUDMCGPDTGAL-----527
 DB 624 VNSIKKYDEVNPNIKIFAVDLEGYKCLNLGDEFENNNYIKIFGMSDILKFIKAKOG 683
 QY 528 ----DVIRNFTLDM 538
 DB 684 ANNVEVIKNFALOKI 698

RESULT 9
 US-10-054-295-52
 ; Sequence 52, Application US/10054295
 ; Patent No. 6921664
 ; GENERAL INFORMATION:
 ; APPLICANT: Cech, Thomas R.
 ; Langer, Joachim
 ; Nakamura, Toru
 ; Chapman, Karen B.
 ; Morin, Gregg B.
 ; Harley, Calvin H.
 ; Andrews, William H.
 ; TITLE OF INVENTION: No. 6921664el Telomerase
 ; NUMBER OF SEQUENCES: 225
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend and Crew LLP
 ; STREET: Two Embarcadero Center, 8th floor
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: United States of America
 ; ZIP: 94111
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: floppy disk
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/10/054,295
 ; FILING DATE: 18-Jan-2002
 ; CLASSIFICATION: 536

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/854,050
 FILING DATE: <Unknown>
 APPLICATION NUMBER: US 08/846,017
 FILING DATE: 25-APR-1997
 APPLICATION NUMBER: US 08/844,419
 FILING DATE: 18-APR-1997
 APPLICATION NUMBER: US 08/724,643
 FILING DATE: 01-OCT-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Apple, Randolph T.
 REGISTRATION NUMBER: 36,429
 REFERENCE/DOCKET NUMBER: 015389-002930US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 TELEFAX: (415) 576-0300
 INFORMATION FOR SEQ ID NO: 52:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 699 amino acids
 TYPE: amino acid
 STRANDEDNESS: <Unknown>
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 SEQUENCE DESCRIPTION: SEQ ID NO: 52:
 US-10-054-295-52

Query Match 6.5%; Score 180.5; DB 2; Length 699;
 Best Local Similarity 20.7%; Pred. No. 3.6e-08;
 Matches 115; Conservative 100; Mismatches 191; Indels 149; Gaps 29;

QY 102 CSDISTQAPFAVEVCRIPHTLFTFIOFKDLKESKCGMGRALAKAIADWTNEKG 161
 DB 175 CTESORCKTMFRYLS-----VTNKQKMDQTKKREKENTLTCL--QAIKESBKSKRETFGD 227
 QY 162 M-----ALALAVTK--YKQRNGMSHKDLRLSHLK-PSSEGLAIVTKYITKGMKEVH 210
 DB 228 IMNVEDAIKALKPAAWKIARQNMK-----KHMKAIPKIPNSTLSKYLT-----FK 275
 QY 211 ELYEKALSVETEKLLKYLEAVEKVKRTKDELEVH-----LIEHRLVHEHLLT 260
 DB 276 DLIFCHISEPERKYKILG--KKYPTKEEYKAFGDSASAPFNPBLAGKMKIEISKI 333
 QY 261 --NHLKSK-----EYWKALL--QEMPLTALLRLGKMTANSVLEPNSSEV--SLVCEKLCN 310
 DB 334 WENELSAKGNATAEVNDNLISNQLPYMMLRNL-----SNLKAGVSDTTHSIVINKICE 388
 QY 311 EKLKKAIRHPHILALETY-----KTGHGIRGL-----KWRPDE 347
 DB 389 PRAVENSIOFPLQFSAIEAVNEAVTKGFKAKKRENNMLKQDIEAVKEVEKTDDEKKDM 448
 QY 348 EILKALDAFYKTFVTEPTGRPL-----LAV-----DVSASMNOR 384
 DB 449 ELEQTEBEF--VKVNEGIGKQYINSIELAIKIAVNNKLDRIKHTAIFSDVSGSMSTS 505
 QY 385 VLGSILNASTVAAAM-----CMVTRTEKDSYVV--AFSDENVPCTVTDM-----428
 DB 506 MSGGAKKYGVSATCECALVIGLAWKORCKESSFYIFSSPSSQCKCYLEVLDLPDGLR 565
 QY 429 TLQOVLAMMSQIPAGTDCSLPMI--MAOKTTPADVTFVFDNTEFTAG-----GVHP 479
 DB 566 SMQKLOEGKGL--GGTDFPYECIDEMT--KNKTHVDNVIYLSDDMIABEYSDINVRGSSI 623
 QY 480 AIALREYRKMDIPAKLIVCGWTSNG--FTIADP--DDRGMUDMCGPDTGAL-----527
 DB 624 VNSIKKYDEVNPNIKIFAVDLEGYKCLNLGDEFENNNYIKIFGMSDILKFIKAKOG 683
 QY 528 ----DVIRNFTLDM 538
 DB 684 ANNVEVIKNFALOKI 698

RESULT 10
 US-09-438-486A-52

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; Sequence 52, Application US/09438486A
; Patent No. 6927285
; GENERAL INFORMATION:
; APPLICANT: CECCH, THOMAS R.
; APPLICANT: LINGNER, JOACHIM
; APPLICANT: NAKAMURA, TORU
; APPLICANT: CHAPMAN, KAREN B.
; APPLICANT: MORIN, GREGG B.
; APPLICANT: HARLEY, CALVIN
; APPLICANT: ANDREWS, WILLIAM H.
; TITLE OF INVENTION: GENE FOR HUMAN TELOMERASE REVERSE TRANSCRIPTASE AND
; FILE REFERENCE: 018/062
; CURRENT APPLICATION NUMBER: US/09/438,486A
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 08/851,843
; PRIOR FILING DATE: 1997-05-06
; PRIOR APPLICATION NUMBER: 08/846,017
; PRIOR FILING DATE: 1997-04-25
; PRIOR APPLICATION NUMBER: 08/844,419
; PRIOR FILING DATE: 1997-04-18
; PRIOR APPLICATION NUMBER: 08/724,643
; PRIOR FILING DATE: 1996-10-01
; NUMBER OF SEQ ID NOS: 223
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 52
; LENGTH: 699
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Recombinant
; OTHER INFORMATION: amino acid sequence
US-09-438-486A-52

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Query Match      6.5%; Score 180.5; DB 2; Length 699;
Best Local Similarity 20.7%; Pred. No. 3.6e-08;
Matches 115; Conservative 100; Mismatches 191; Indels 149; Gaps 29;

Cy 102 CSDISTQAAKAVSEVCRIPTHLFTPIQPKDKESKCMGMRALRKALADWYNEKG 161
Db 175 CTESQRRKTMFRYLS-----VTNRQKWDQTKRKRKNLITL--QAIKESDCKRRETD 227
Cy 162 M-----ALALAVTK--YKQRNGWSHKDLRLSLHK-PSEGLAIVTYITKGWKEVH 210
Db 228 IMNVEDAIKALKAPVAKKIAGKQNAK-----KHMARPIPNSTLESKITL-----FK 275
Cy 211 ELYEKALSVETKLLKYLAEVKKVTKDELEVH-----LIEHRVLVREHLLT 260
Db 276 DLIRCHISSEPKERYKITLG--KKYPTKEEYKAAFQDSASAPNPBLAGRMKLEISK 333
Cy 261 --NHLSK---EYWKALL--QEMPLTLLNLGKMTANSVLEPGNSEV--SLYCEKLCN 310
Db 334 WENELISAGNTAEVWDNLISNQLPYMAMLRNL-----SNLIKAGVSDTSHIVINKICE 388
Cy 311 EKLKKARIHPHILIALEY-----KTGHGIRGL-----KMRPDE 347
Db 389 PKAVENSGMFPLOFSAIEAVNEATKGFYKAKKRNMLKQDIAVKEVVEKTBKEDKM 448
Cy 348 EILKALDAAFYKTEKTEPGRFL--LAV-----DVSAWNR 384
Db 449 ELBQTEBEGF--VKVNGIGIGQYINSIELAIKIAVNKNLDEIKGHTAIFSDVSGSMSTS 505
Cy 385 VLGSILNASTAAAM-----CMVTTRTEKDSYV--AFSDENVPCVTTDM-----428
Db 506 MSGAKKTYGVRTCECALVGLMWKQRCESKFYIFSSPSCQKCYLAEVLDLPDELRP 565
Cy 429 TLQGVAMSGDIPRGTCDSLPMI--MAQKNTPADVIVFTDNTFAG-----GVHP 479
Db 566 SMQKLLQKGL--GGGTFPYECIDEMT--KXKTHVDNVIILSDMMIAEGYDINVRGSI 623
Cy 480 AIAAREYKRDMDIPAKLIVCGTSSNG--FTIADP--DDRGMLDMCGFDTGAL-----527
Db 624 VNSIKKYDEVNPNKIKIPAVLDLEGYKGLNLDENENNYYIKIFQMSDILKFTISAKGG 683

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Cy 528 ----DVIRNFTLDMI 538
Db 684 ANNVEYIKNPLAKKI 698

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RESULT 11
US-08-851-843A-7
; Sequence 7, Application US/08851843A
; Patent No. 6093809
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: No. 6093809el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/851,843A
; FILING DATE: 06-MAY-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 719 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
; US-08-851-843A-7

Query Match      6.5%; Score 180.5; DB 2; Length 719;
Best Local Similarity 20.7%; Pred. No. 3.8e-08;
Matches 115; Conservative 100; Mismatches 191; Indels 149; Gaps 29;

Cy 102 CSDISTQAAKAVSEVCRIPTHLFTPIQPKDKESKCMGMRALRKALADWYNEKG 161
Db 193 CTESQRRKTMFRYLS-----VTNRQKWDQTKRKRKNLITL--QAIKESDCKRRETD 245
Cy 162 M-----ALALAVTK--YKQRNGWSHKDLRLSLHK-PSEGLAIVTYITKGWKEVH 210

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Db      : 246  I M N V E D A I K A L K P A V M K K I A R Q N A M K ----- K H M A P K I P N S T L S K V I T ----- F K 293
Qy      : 211  E L Y K E K A L S V E T E K L K Y L E A V E K V K R T K D E L E V I H ----- L I E H R L V R E H L I T 260
Db      : 294  D L I F C H I S E P K E R E Y K I L G -- K K Y P K T E E B E Y K A F G D S A S A P F N P E L A G R M K I E I S K T 351
Qy      : 261  -- N H L K S K ----- E W K A L L -- Q E M P L T A L L N L G M T A N S V L E P G N S E V -- S L V C E K I C N 310
Db      : 352  W E N E L S A G N T A E V D N L I S S N Q L P Y M A M L R N L ----- S N I L K A G V S D T T H S I V I N K I C E 406
Qy      : 311  E K L K K A R I H P H I L I A L E T Y ----- K T G H G I R G K L ----- K W R P D E 347
Db      : 407  P R A V E N S K M P L O P F S A I E A V N E A V T K G P K A K R E N N L K G O I E A V K E V E K T D E E K K O M 466
Qy      : 348  E I L K A L D A A F Y K T F P T V E P T G R F L ----- L A V ----- D V S A S M A N O R 384
Db      : 467  E L E G T E E B E F ----- V K V N G I G I G O Y I N S I E L A I K I A V N K N L D E I K G H T A I F S D V S G S M S T S 523
Qy      : 385  V L G S I L A N S T V A A A M ----- C M V T R T E K D S Y V V -- A F S D E M V P C V T T D M ----- 428
Db      : 524  M S G A K K Y G S V R T C E A L V I G I A M V K O R C E K S S F Y I F S S P S Q C N K C Y L E V D L P E D E L R P 583
Qy      : 429  T L Q O V L A M S Q I P A G T D C S L P M I -- W A Q K T T P A D V E I V F T D N E T F A G ----- G V H P 479
Db      : 584  S M O K L O E R K G L -- G G T D P P Y E C I D E W T -- K N K T H V D N I V I L S D M M I A G Y S D I N V R G S S I 641
Qy      : 480  A I A L E Y E R K K D I P A K L I V C G M T S N G -- F T I A D P -- D R G M L D M C G F D T G A L ----- 527
Db      : 642  V N S I K Y K D E V N P N K I F A V D L E G Y G K C L A N L D B E N N E N N Y I K I F M S D S I L K F I S A K O G 701
Qy      : 528  --- D V I R N F T L D M I 538
Db      : 702  A N M V E V I K N P A L O K I 716

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RESULT 12
US-08-974-549A-219
Sequence 219, Application US/08974549A
Patent No. 6166178

GENERAL INFORMATION:

APPLICANT: Czech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Human telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
PRIOR APPLICATION DATA:

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APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 219:
SEQUENCE CHARACTERISTICS:
LENGTH: 719 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-974-549A-219

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Query Match 6.5%; Score 180.5; DB 2; Length 719;
Best Local Similarity 20.7%; Pred. No. 3.8e-08;
Matches 115; Conservative 100; Mismatches 191; Indels 149; Gaps 29;

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Qy      102  C S D I S T Q A F R A V E S E V R I P T H L T F I O F K K D L K E S K C G M W G R L A K A I A D A T Y N E K G 161
Db      193  C T E S Q R K K T M F R Y L S ----- V T N K O K W O T K K G K R E N L I T K L -- O A I E S E K S G R E T G D 245
Qy      162  M ----- A L A V T K -- Y K O R N G S H K D L R L S H L K - P S E G I A I V T K Y I T K G M K E V H 210
Db      246  I M N V E D A I K A L K P A V M K K I A R Q N A M K ----- K H M A P K I P N S T L S K V I T ----- F K 293
Qy      211  E L Y K E K A L S V E T E K L K Y L E A V E K V K R T K D E L E V I H ----- L I E H R L V R E H L I T 260
Db      294  D L I F C H I S E P K E R E Y K I L G -- K K Y P K T E E B E Y K A F G D S A S A P F N P E L A G R M K I E I S K T 351
Qy      261  -- N H L K S K ----- E W K A L L -- Q E M P L T A L L N L G M T A N S V L E P G N S E V -- S L V C E K I C N 310
Db      352  W E N E L S A G N T A E V D N L I S S N Q L P Y M A M L R N L ----- S N I L K A G V S D T T H S I V I N K I C E 406
Qy      311  E K L K K A R I H P H I L I A L E T Y ----- K T G H G I R G K L ----- K W R P D E 347
Db      407  P R A V E N S K M P L O P F S A I E A V N E A V T K G P K A K R E N N L K G O I E A V K E V E K T D E E K K O M 466
Qy      348  E I L K A L D A A F Y K T F P T V E P T G R F L ----- L A V ----- D V S A S M A N O R 384
Db      467  E L E G T E E B E F ----- V K V N G I G I G O Y I N S I E L A I K I A V N K N L D E I K G H T A I F S D V S G S M S T S 523
Qy      385  V L G S I L A N S T V A A A M ----- C M V T R T E K D S Y V V -- A F S D E M V P C V T T D M ----- 428
Db      524  M S G A K K Y G S V R T C E A L V I G I A M V K O R C E K S S F Y I F S S P S Q C N K C Y L E V D L P E D E L R P 583
Qy      429  T L Q O V L A M S Q I P A G T D C S L P M I -- W A Q K T T P A D V E I V F T D N E T F A G ----- G V H P 479
Db      584  S M O K L O E R K G L -- G G T D P P Y E C I D E W T -- K N K T H V D N I V I L S D M M I A G Y S D I N V R G S S I 641

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QY 480 AIALREYRKMDIPAKLIVCGMTSNG--FTIADP-DDRGMLDMCGFPTGAL----- 527
 Db 642 VNSIKKTKDEVNPIKIFAVDLBGYGKCLMGDEFENNNYIKIFGMSDILKFIASAKOG 701
 QY 528 ----DVIRNFTLDMI 538
 Db 702 ANNVEVIKNFALOKI 716

RESULT 13
 US-08-854-050-7
 ; Sequence 7, Application US/08854050
 ; Patent No. 6261836

GENERAL INFORMATION:
 APPLICANT: Cech, Thomas R.
 APPLICANT: Lingner, Joachim
 APPLICANT: Nakamura, Toru
 APPLICANT: Chapman, Karen B.
 APPLICANT: Morin, Gregg B.
 APPLICANT: Harley, Calvin
 APPLICANT: Andrews, William H.
 TITLE OF INVENTION: No. 6261836el Telomerase
 NUMBER OF SEQUENCES: 225
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, 8th Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: United States of America
 ZIP: 94111

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/854,050
 FILING DATE: 09-MAY-1997
 CLASSIFICATION: 536
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/851,843
 FILING DATE: 06-MAY-1997
 CLASSIFICATION: 536
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/846,017
 FILING DATE: 25-APR-1997
 CLASSIFICATION: 536
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/844,419
 FILING DATE: 18-APR-1997
 CLASSIFICATION: 536
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/724,643
 FILING DATE: 01-OCT-1996
 CLASSIFICATION: 536
 ATTORNEY/AGENT INFORMATION:
 NAME: Apple, Randolph T.
 REGISTRATION NUMBER: 36,429
 REFERENCE/DOCKET NUMBER: 015389-002930US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 TELEFAX: (415) 576-0300
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 719 amino acids
 TYPE: amino acid
 STRANDEDNESS: not relevant
 TOPOLOGY: not relevant
 MOLECULE TYPE: protein
 US-08-854-050-7

Query Match 6.5%; Score 180.5; DB 2; Length 719;

Best Local Similarity 20.7%; Pred. No. 3.8e-08;
 Matches 115; Conservative 100; Mismatches 191; Indels 149; Gaps 29;

QY 102 CSDISTKQAAFKAVSEVCRIFPTLFTFIOFKDLKSKMKCGMMGRALRAIADVYNGKG 161
 Db 193 CTESQKTKMFRYLS-----VTNKQKMDYTKKREKLTLYL--QATKSESDSKRETGD 245
 QY 162 M-----ALALAVTK--YKQRNGWSHKDLRLSHLK-PSSEGLAVTYTITGKWEVH 210
 Db 246 INNVEDAIALKLRVAVKIKIAKRONAK-----KHKAKKINSITLESKYL-----FK 293
 QY 211 ELYEKALSVETKLKYLEAVEKVKRTKDELEVIH-----LIEHRLVREHLIT 260
 Db 294 DLIKFCHISPKERVYKILG--KKYPTKEEYKAAFGDSASAPFNPLAKGRMKIERISK 351
 QY 261 --NHLSK-----EVRKALL--QEMPLTALRLNGKMTANSVLBGNSEV--SLVCEKLCN 310
 Db 352 WEWELSAKGNATAEVMDLISSNQLPYVAMLRNL-----SNILKAGVSDTTHSHVINKICE 406
 QY 311 EKLTKARIRHPHILALLETY-----KTGHLRGKL-----KWRPDE 347
 Db 407 PKAVENSKMFPPLQFSLAEAVNEAVTKGFKAQKRENNNLGQILEAVKVEKTDDEKKDM 466
 QY 348 EILKALDAFYKTKFVPTGKRFPL--LAV-----DVSASANOR 384
 Db 467 ELQTEGEGF--VKVNEGIGKOYINSIBLAIKIAVNKNLDEIKGHTAIFSDVSGSMSTS 523
 QY 385 VLGSILNASTVNAAM-----GMVVTREKDSYVV--AFSDEWVPCVPTTDM----- 428
 Db 524 MSGAKKYGVSVRTLCBICALVGLMVKORCEKSSFYIFSSPSQCNKCYLEVDLFGDELRL 583
 QY 429 TLQOVLMAMSGIIPAGTDCSLPMI--WAQKTNTPADVIFVTNETPAG-----GVHP 479
 Db 584 SMQKLGKRGKL--GGGTDFPEYECIDEWT--KQKHVNDIVILSDMMIABGSDIIVRSSSI 641
 QY 480 AIALREYRKMDIPAKLIVCGMTSNG--FTIADP-DDRGMLDMCGFPTGAL----- 527
 Db 642 VNSIKKTKDEVNPIKIFAVDLBGYGKCLMGDEFENNNYIKIFGMSDILKFIASAKOG 701
 QY 528 ----DVIRNFTLDMI 538
 Db 702 ANNVEVIKNFALOKI 716

RESULT 14
 US-09-430-323-7
 ; Sequence 7, Application US/09430323
 ; Patent No. 6309867

GENERAL INFORMATION:
 APPLICANT: Cech, Thomas R.
 APPLICANT: Lingner, Joachim
 APPLICANT: Nakamura, Toru
 APPLICANT: Chapman, Karen B.
 APPLICANT: Morin, Gregg B.
 APPLICANT: Harley, Calvin
 APPLICANT: Andrews, William H.
 TITLE OF INVENTION: No. 6309867el Telomerase
 NUMBER OF SEQUENCES: 225
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, 8th Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: United States of America
 ZIP: 94111

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/430,323
 FILING DATE: 29-Oct-1999

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CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US 08/854,050
  FILING DATE: 09-MAY-1997
  APPLICATION NUMBER: US 08/851,843
  FILING DATE: 06-MAY-1997
  APPLICATION NUMBER: US 08/846,017
  FILING DATE: 25-APR-1997
  APPLICATION NUMBER: US 08/844,419
  FILING DATE: 18-APR-1997
  APPLICATION NUMBER: US 08/724,643
  FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
  NAME: Apple, Randolph T.
  REGISTRATION NUMBER: 36,429
  REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
  TELEPHONE: (415) 576-0200
  TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 7:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 719 amino acids
    TYPE: amino acid
    STRANDNESS: not relevant
    TOPOLOGY: not relevant
    MOLECULE TYPE: protein
    SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-430-323-7

Query Match      6.5% Score 180.5: DB 2: Length 719:
Best Local Similarity 20.7%: Pred. No. 3.8e-08:
Matches 115: Conservative 100: Mismatches 191: Indels 149: Gaps 29:

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RESULT 15
US-09-402-181B-219
  Sequence 219, Application US/09402181B
  Patent No. 6610839
  GENERAL INFORMATION:
    APPLICANT: Cech, Thomas R.
    Inventor: Cech, Thomas R.
    Nakamura, Toru
    Chapman, Karen B.
    Morin, Gregg B.
    Harley, Calvin B.
    Andrews, William H.
  TITLE OF INVENTION: Human Telomerase Catalytic Subunit
  NUMBER OF SEQUENCES: 633
  CORRESPONDENCE ADDRESS:
    ADDRESSEE: Townsend and Townsend and Crew LLP
    STREET: Two Embarcadero Center, Eighth Floor
    CITY: San Francisco
    STATE: California
    COUNTRY: USA
    ZIP: 94111-3834
  COMPUTER READABLE FORM:
    MEDIUM TYPE: floppy disk
    COMPUTER: IBM PC compatible
    OPERATING SYSTEM: PC-DOS/MS-DOS
    SOFTWARE: PatentIn Release #1.0, Version #1.30
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/09/402,181B
    FILING DATE: 29-Sep-1997
    CLASSIFICATION: <Unknown>
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: US 08/724,643
    FILING DATE: 01-OCT-1996
    APPLICATION NUMBER: US 08/844,419
    FILING DATE: 18-APR-1997
    APPLICATION NUMBER: US 08/846,017
    FILING DATE: 25-APR-1997
    APPLICATION NUMBER: US 08/851,843
    FILING DATE: 06-MAY-1997
    APPLICATION NUMBER: US 08/854,050
    FILING DATE: 09-MAY-1997
    APPLICATION NUMBER: US 08/911,312
    FILING DATE: 14-AUG-1997
    APPLICATION NUMBER: US 08/912,951
    FILING DATE: 14-AUG-1997
    APPLICATION NUMBER: US 08/915,503
    FILING DATE: 14-AUG-1997
    APPLICATION NUMBER: WO PCT/US97/17885
    FILING DATE: 01-OCT-1997
  ATTORNEY/AGENT INFORMATION:
    NAME: Ausubius, Scott L.
    REGISTRATION NUMBER: 42,271
    REFERENCE/DOCKET NUMBER: 015389-002620US
  TELECOMMUNICATION INFORMATION:
    TELEPHONE: (415) 576-0200
    TELEFAX: (415) 576-0300
  INFORMATION FOR SEQ ID NO: 219:
    SEQUENCE CHARACTERISTICS:
      LENGTH: 719 amino acids
      TYPE: amino acid
      TOPOLOGY: linear
    MOLECULE TYPE: protein
    SEQUENCE DESCRIPTION: SEQ ID NO: 219:
US-09-402-181B-219

Query Match      6.5% Score 180.5: DB 2: Length 719:
Best Local Similarity 20.7%: Pred. No. 3.8e-08:
Matches 115: Conservative 100: Mismatches 191: Indels 149: Gaps 29:

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OY 162 M-----ALALATK--YKORNGSHODLRSLHTK--PSEBGLAIYKTKITKGKEVN 210
Db 246 IMNVEDAIKALPRAWMKIYAKRONAMK-----KMKKAPKIPNSTLBSYITL-----FK 293
OY 241 ELYEKALSVETEKLLKYLEAVEKVYKTYODELEVIH-----LIBEHLVREHLIT 260
Db 294 DLIKCHISEPERVYKIIG--KKYKYTEEEYKAFGDSASAPFDELAKRKRIEISKT 351
OY 261 --NHLKSK-----EWKALL--QEMPLTALLRYNGKMTASVLEPGNSEV--SLYCEKLN 310
Db 352 WENELISAKGNTAEVWDNLSSNOLPYMALRNL-----SNILAGSVDTTHSTIVINKICE 406
OY 311 EKLTKKARIHPHILITALETY-----KTGHGRGKLT-----KMRPDE 347
Db 407 PKAVENSMKMFLOQPSAISAEVAVNEAVTKGPKAKKREMNLIKQLEAVEKEVEKTEDEKKOM 466
OY 348 EILKLDAAFYTEKTEVPTGKRL--LAV-----DYSABMNQR 384
Db 467 ELEQTEEGEF--VKRNEBGIKROYINSIELATIKAVKNLDEIKGHTAIPSDVSGSGMSTS 523
OY 365 VLGSITINASTVAAAM-----CMVTRTEKDSYVV--AFSDMEVPCPYTTDM-----428
Db 524 MSGGAKKXGVSATCJECALVILGIMVYQROBKESFYIFSSPSSGCKNYCLEVLDLPGDELRE 583
OY 429 TLQOVLAMASQIPAGTDCSLPMI--WAOQKTPADVFIYFTDNEFPAG-----GVHP 479
Db 584 SMQKLLQOEKGKLI--GGGTDPPEYCEIDEMT--KNKTHVNIYILSDMTAEGSGIDINVRGSSI 641
OY 480 AIALREYRKMDIPAKLIYCGMTSNG--FTIADP--DDRGMILDMDCGFDTCAL-----527
Db 642 VNSIKKYKDEAVNPNIKIFAVNDELEGYCKNLGDEFENNYIYIKIFGMSDSLTKRTSAKGGG 701
OY 528 ---DVIRNFTLDMI 538
Db 702 ANMVEVIRKIFALOKI 716

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Search completed: January 13, 2006, 11:11:50
Job time : 28 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 13, 2006, 11:10:45 ; Search time 116 Seconds
(without alignments)
1937.864 Million cell updates/sec

Title: US-10-615-515-6

Perfect score: 2787
Sequence: 1 MESSVNQMPLEKQIANSQ.....MCGFDTGALDIVRNFTLDMT 538

Scoring table:
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA_Main:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2787	100.0	538	4	US-10-615-515-6 Sequence 6, App1
2	2787	100.0	538	4	US-10-788-792-196 Sequence 196, App
3	2787	100.0	552	4	US-10-288-858-1 Sequence 1, App1
4	2782	99.8	553	4	US-10-288-858-2 Sequence 2, App1
5	2782	99.8	553	4	US-10-288-858-6 Sequence 6, App1
6	2522.5	90.5	537	4	US-10-615-515-10 Sequence 10, App1
7	2269	81.4	538	4	US-10-615-515-11 Sequence 11, App1
8	1011	36.3	643	4	US-10-615-515-12 Sequence 12, App1
9	185.5	6.7	641	6	US-11-097-143-5949 Sequence 5949, Ap
10	180.5	6.5	699	3	US-09-843-676-52 Sequence 52, App1
11	180.5	6.5	699	3	US-09-766-253-52 Sequence 52, App1
12	180.5	6.5	699	3	US-09-438-486-52 Sequence 52, App1
13	180.5	6.5	699	4	US-10-053-758-52 Sequence 52, App1
14	180.5	6.5	699	4	US-10-054-295-52 Sequence 52, App1
15	180.5	6.5	699	4	US-10-054-611-52 Sequence 52, App1
16	180.5	6.5	699	4	US-10-325-810-188 Sequence 188, App
17	180.5	6.5	699	5	US-10-877-124-188 Sequence 188, App
18	180.5	6.5	699	5	US-10-877-022-188 Sequence 188, App
19	180.5	6.5	699	5	US-10-877-146-188 Sequence 188, App
20	180.5	6.5	719	3	US-09-843-676-52 Sequence 7, App1
21	180.5	6.5	719	3	US-09-766-253-7 Sequence 7, App1
22	180.5	6.5	719	3	US-09-438-486-7 Sequence 7, App1
23	180.5	6.5	719	4	US-10-053-758-7 Sequence 7, App1
24	180.5	6.5	719	4	US-10-054-295-7 Sequence 7, App1
25	180.5	6.5	719	4	US-10-054-611-7 Sequence 7, App1
26	180.5	6.5	719	4	US-10-325-810-219 Sequence 219, App
27	180.5	6.5	719	5	US-10-877-124-219 Sequence 219, App

28	180.5	6.5	719	5	US-10-877-022-219 Sequence 219, App
29	180.5	6.5	719	5	US-10-877-146-219 Sequence 219, App
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31	130.5	4.7	1937	5	US-10-723-860-106 Sequence 106, App
32	123	4.4	23	4	US-10-376-121A-48 Sequence 48, App1
33	120.5	4.3	720	4	US-10-437-963-167109 Sequence 167109, A
34	120	4.3	824	4	US-10-108-260A-4573 Sequence 4573, Ap
35	120	4.3	892	4	US-10-205-219-102 Sequence 102, App
36	119.5	4.3	876	5	US-10-723-860-60 Sequence 60, App1
37	116	4.2	22	4	US-10-376-121A-55 Sequence 55, App1
38	116	4.2	1177	5	US-10-732-923-3293 Sequence 3293, Ap
39	115.5	4.1	550	4	US-10-104-047-3495 Sequence 3495, A
40	115.5	4.1	571	4	US-10-122A-77167 Sequence 77167, A
41	115	4.1	561	3	US-09-895-913A-334 Sequence 334, App
42	114.5	4.1	1128	5	US-10-732-923-3117 Sequence 3117, Ap
43	114.5	4.1	1418	4	US-10-368-493-22315 Sequence 22315, A
44	113.5	4.1	2025	4	US-10-788-792-180 Sequence 180, App
45	113	4.1	1577	4	US-10-369-493-6924 Sequence 6924, Ap

ALIGNMENTS

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RESULT 1
US-10-615-515-6
; Sequence 6, Application US/10615515
; General Information:
; PUBLIC INFORMATION:
; APPLICATION: FAGAN, RICHARD, JOSEPH
; APPLICANT: PHELPS, CHRISTOPHER BENJAMIN
; APPLICANT: GUTTERIDGE, ALEX
; TITLE OF INVENTION: ADHESION MOLECULES
; FILE REFERENCE: 674575-2004
; CURRENT APPLICATION NUMBER: US/10/615,515
; PRIOR FILING DATE: 2003-07-08
; PRIOR APPLICATION NUMBER: PCT/GB02/00107
; PRIOR FILING DATE: 2002-01-11
; PRIOR APPLICATION NUMBER: GB 0100750.9
; PRIOR FILING DATE: 2001-01-11
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 6
; LENGTH: 538
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-615-515-6

Query Match      100.0%; Score 2787; DB 4; Length 538;
Best Local Similarity 100.0%; Pred. No. 2.4e-243;
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB      1 MESSVNQMPLEKQIANSQDGYVQVDMNHLRFLCGSEGGTYIYKQKLGLENAA 60

QY      61 LRLLEDGCGCAVIOEIKFSQSEGRITQEPMLFALICQSDSISTQAAKRAVSEVR 120
DB      61 LRLLEDGCGCAVIOEIKFSQSEGRITQEPMLFALICQSDSISTQAAKRAVSEVR 120

QY      121 IPTHLEFTFIOFKKDKESKCGMMGRALRKALADWYNEKGNALAVTKYKORNGMSHK 180
DB      121 IPTHLEFTFIOFKKDKESKCGMMGRALRKALADWYNEKGNALAVTKYKORNGMSHK 180

QY      181 DILRLSHLKPSSSEGLAIVTKYITKGKEVHELYKEXALSVETBKLIKTYEAVERKARTD 240
DB      181 DILRLSHLKPSSSEGLAIVTKYITKGKEVHELYKEXALSVETBKLIKTYEAVERKARTD 240

QY      241 ELLEVHLIIEHRLVREHLLTNHLKSKYEWKALLOEMPTLALRNIGKMTANSVLEBGNSE 300
DB      241 ELLEVHLIIEHRLVREHLLTNHLKSKYEWKALLOEMPTLALRNIGKMTANSVLEBGNSE 300

QY      301 VSLVEKICNEKLLKKKARIHPHILIALETYKYGIRGKLKMRPDEBITKALDAAFYK 360
DB      301 VSLVEKICNEKLLKKKARIHPHILIALETYKYGIRGKLKMRPDEBITKALDAAFYK 360
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Db 301 VSLVCEKLCNEKLLKKARLHPHLLALETKYTGHLRGKLRKWRPDEEILKALDAAFYKT 360
 Qy 361 FKTYEPGKRFLLAVDVASASNNQVLSIINASTVAAAMCMVTRTERKDSYVAFSDENV 420
 Db 361 FKTYEPGKRFLLAVDVASASNNQVLSIINASTVAAAMCMVTRTERKDSYVAFSDENV 420
 Qy 421 PCPVTMTLQOVVMAASQIPAGGTDGSLPMIWAQKNTPADVFIVFTDNETFAGGVHFA 480
 Db 421 PCPVTMTLQOVVMAASQIPAGGTDGSLPMIWAQKNTPADVFIVFTDNETFAGGVHFA 480
 Qy 481 IALREYRKMDIPAKLIIVCGMTSNGFTIADPDDRGMLDMCGFDGALDVIRNFTLDMI 538
 Db 481 IALREYRKMDIPAKLIIVCGMTSNGFTIADPDDRGMLDMCGFDGALDVIRNFTLDMI 538

RESULT 2
 US-10-788-792-196
 ; Sequence 196, Application US/10788792
 ; Publication No. US20040191819A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bayer Pharmaceuticals Corporation
 ; APPLICANT: Evelygh, Deepa
 ; APPLICANT: Bigwood, Douglas
 ; TITLE OF INVENTION: EXPRESSION PROFILES FOR BREAST CANCER AND METHODS OF USE
 ; FILE REFERENCE: 5152
 ; CURRENT APPLICATION NUMBER: US/10/788, 792
 ; CURRENT FILING DATE: 2004-02-27
 ; PRIOR APPLICATION NUMBER: US 60/450,655
 ; PRIOR FILING DATE: 2003-02-28
 ; NUMBER OF SEQ ID NOS: 254
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 196
 ; LENGTH: 538
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-788-792-196

Query Match 100.0%; Score 2787; DB 4; Length 538;
 Best Local Similarity 100.0%; Pred. No. 2.4e-243;

Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 1 MESSVNQMPLEKQIANSQDGYVQVTDNRRLHFLCFSGEGTYYIKQKGLNENAE 60
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 Db 61 LIRLIEDRGCEVIOEIKSFQSGRTTKQEPMLPALAICQCSISTKQAAFVSEYCR 120
 Qy 121 IPTHLFTFIQPKDKESMKCGMGRALRAKAIADWYNEKGMALALAVTKYKORNGSHK 180
 Db 121 IPTHLFTFIQPKDKESMKCGMGRALRAKAIADWYNEKGMALALAVTKYKORNGSHK 180
 Qy 181 DLRLSHLKPSSGLAVTKYITKGKVEHLYEKKALSVETEKLLKYLEAVEKVKRTKD 240
 Db 181 DLRLSHLKPSSGLAVTKYITKGKVEHLYEKKALSVETEKLLKYLEAVEKVKRTKD 240
 Qy 241 ELAVYHLIEBRLVREHLLTNHLKSKEVWKLLOEMPLTALLRLNGKMTANSVLEPGNSE 300
 Db 241 ELAVYHLIEBRLVREHLLTNHLKSKEVWKLLOEMPLTALLRLNGKMTANSVLEPGNSE 300
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 Db 301 VSLVCEKLCNEKLLKKARLHPHLLALETKYTGHLRGKLRKWRPDEEILKALDAAFYKT 360
 Qy 361 FKTYEPGKRFLLAVDVASASNNQVLSIINASTVAAAMCMVTRTERKDSYVAFSDENV 420
 Db 361 FKTYEPGKRFLLAVDVASASNNQVLSIINASTVAAAMCMVTRTERKDSYVAFSDENV 420
 Qy 421 PCPVTMTLQOVVMAASQIPAGGTDGSLPMIWAQKNTPADVFIVFTDNETFAGGVHFA 480
 Db 421 PCPVTMTLQOVVMAASQIPAGGTDGSLPMIWAQKNTPADVFIVFTDNETFAGGVHFA 480

Qy 481 IALREYRKMDIPAKLIIVCGMTSNGFTIADPDDRGMLDMCGFDGALDVIRNFTLDMI 538
 Db 481 IALREYRKMDIPAKLIIVCGMTSNGFTIADPDDRGMLDMCGFDGALDVIRNFTLDMI 538

RESULT 3
 US-10-288-858-1
 ; Sequence 1, Application US/10288858
 ; Publication No. US20030109001A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Burekhardt, Jean
 ; APPLICANT: Haas, Michael
 ; APPLICANT: Lehmann, Hans-Peter
 ; TITLE OF INVENTION: Process for the Recombinant Production of Ribonucleoproteins
 ; FILE REFERENCE: RDID 0052US
 ; CURRENT APPLICATION NUMBER: US/10/288, 858
 ; CURRENT FILING DATE: 2002-11-06
 ; PRIOR APPLICATION NUMBER: DE 19931380.6
 ; PRIOR FILING DATE: 1999-07-07
 ; NUMBER OF SEQ ID NOS: 14
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 1
 ; LENGTH: 552
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; NAME/KEY: mic.feature
 ; OTHER INFORMATION: SSAG6 M4-C6
 ; US-10-288-858-1

Query Match 100.0%; Score 2787; DB 4; Length 552;
 Best Local Similarity 100.0%; Pred. No. 2.5e-243;
 Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 73 LIRLIEDRGCEVIOEIKSFQSGRTTKQEPMLPALAICQCSISTKQAAFVSEYCR 132
 Qy 181 DLRLSHLKPSSGLAVTKYITKGKVEHLYEKKALSVETEKLLKYLEAVEKVKRTKD 240
 Db 193 DLRLSHLKPSSGLAVTKYITKGKVEHLYEKKALSVETEKLLKYLEAVEKVKRTKD 252
 Qy 241 ELAVYHLIEBRLVREHLLTNHLKSKEVWKLLOEMPLTALLRLNGKMTANSVLEPGNSE 300
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 Db 493 IALREYRKMDIPAKLIIVCGMTSNGFTIADPDDRGMLDMCGFDGALDVIRNFTLDMI 550

RESULT 4
 US-10-288-858-2

Sequence 2, Application US/10288858
 Publication No. US20030109001A1
 GENERAL INFORMATION:
 APPLICANT: Burchardt, Jean
 APPLICANT: Haase, Michael
 APPLICANT: Lehmann, Hans-Peter
 TITLE OF INVENTION: Process for the Recombinant Production of Ribonucleoproteins
 FILE REFERENCE: RDID 005205
 CURRENT APPLICATION NUMBER: US/10/288,858
 CURRENT FILING DATE: 2002-11-06
 PRIOR APPLICATION NUMBER: DE 19931380.6
 PRIOR FILING DATE: 1999-07-07
 NUMBER OF SEQ ID NOS: 14
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO 2
 LENGTH: 553
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: misc_feature
 OTHER INFORMATION: SSA60 M56
 US-10-288-858-2

Query Match 99.8%; Score 2782; DB 4; Length 553;
 Best Local Similarity 100.0%; Pred. No. 7,1e-243; Indels 0; Gaps 0;
 Matches 537; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 QY 62 IRLIEDGRCCEVIQRIKSPQSGRTTKQEPMLPALAISCQSDISTKQAAFAVSEVCRI 121
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 QY 122 PTHLFTPIQPKDLESMKCGMGRALRKATADWNEKGMAALAAVTKYKORNGMSHD 181
 DB 137 PTHLFTPIQPKDLESMKCGMGRALRKATADWNEKGMAALAAVTKYKORNGMSHD 196
 QY 192 LRLSHLKPSSEGLAVTKYITKGMEVHELYKEKALSVETEKLYLEAVEKVKRTQDE 241
 DB 197 LRLSHLKPSSEGLAVTKYITKGMEVHELYKEKALSVETEKLYLEAVEKVKRTQDE 256
 QY 242 LEVHILIEBHRLVREHLITNHLKSKVWKALLOEMPLTALLNLGKMTANSVLEPNSSEV 301
 DB 257 LEVHILIEBHRLVREHLITNHLKSKVWKALLOEMPLTALLNLGKMTANSVLEPNSSEV 316
 QY 302 SLVCEKLCNEKLLKARHHPHILLALETYKTGHGRLGRLKMRPDEILKALDAAFYKTF 361
 DB 317 SLVCEKLCNEKLLKARHHPHILLALETYKTGHGRLGRLKMRPDEILKALDAAFYKTF 376
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 DB 377 KTVPEPTGRFLAADVSAAMNORVLGSIINASTVAAMCMVTRTEKDSYVAAFSDENVP 436
 QY 422 CPVTTDMTLQOVLAMASQIPAGGTDCLPMIWAQKNTNPADVFIYFTDNETPAGGVHPAI 481
 DB 437 CPVTTDMTLQOVLAMASQIPAGGTDCLPMIWAQKNTNPADVFIYFTDNETPAGGVHPAI 496
 QY 482 ALREYRKQNDIPAKLIVCGMTSNGFTIADPDDRGMLDMCGFDTGALDVIRNFTLDMI 538
 DB 497 ALREYRKQNDIPAKLIVCGMTSNGFTIADPDDRGMLDMCGFDTGALDVIRNFTLDMI 553

RESULT 5
 US-10-288-858-6
 Sequence 6, Application US/10288858
 Publication No. US20030109001A1
 GENERAL INFORMATION:
 APPLICANT: Burchardt, Jean
 APPLICANT: Haase, Michael
 APPLICANT: Lehmann, Hans-Peter
 TITLE OF INVENTION: Process for the Recombinant Production of Ribonucleoproteins

FILE REFERENCE: RDID 005205
 CURRENT APPLICATION NUMBER: US/10/288,858
 CURRENT FILING DATE: 2002-11-06
 PRIOR APPLICATION NUMBER: DE 19931380.6
 PRIOR FILING DATE: 1999-07-07
 NUMBER OF SEQ ID NOS: 14
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO 6
 LENGTH: 553
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-288-858-6

Query Match 99.8%; Score 2782; DB 4; Length 553;
 Best Local Similarity 100.0%; Pred. No. 7,1e-243; Indels 0; Gaps 0;
 Matches 537; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EESVQMPLENEKQIANSODGYVQVTDNRLHRLCFSGSEGTYIYKEOKLGENAEAL 61
 DB 17 EESVQMPLENEKQIANSODGYVQVTDNRLHRLCFSGSEGTYIYKEOKLGENAEAL 76
 QY 62 IRLIEDGRCCEVIQRIKSPQSGRTTKQEPMLPALAISCQSDISTKQAAFAVSEVCRI 121
 DB 77 IRLIEDGRCCEVIQRIKSPQSGRTTKQEPMLPALAISCQSDISTKQAAFAVSEVCRI 136
 QY 122 PTHLFTPIQPKDLESMKCGMGRALRKATADWNEKGMAALAAVTKYKORNGMSHD 181
 DB 137 PTHLFTPIQPKDLESMKCGMGRALRKATADWNEKGMAALAAVTKYKORNGMSHD 196
 QY 192 LRLSHLKPSSEGLAVTKYITKGMEVHELYKEKALSVETEKLYLEAVEKVKRTQDE 241
 DB 197 LRLSHLKPSSEGLAVTKYITKGMEVHELYKEKALSVETEKLYLEAVEKVKRTQDE 256
 QY 242 LEVHILIEBHRLVREHLITNHLKSKVWKALLOEMPLTALLNLGKMTANSVLEPNSSEV 301
 DB 257 LEVHILIEBHRLVREHLITNHLKSKVWKALLOEMPLTALLNLGKMTANSVLEPNSSEV 316
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 DB 377 KTVPEPTGRFLAADVSAAMNORVLGSIINASTVAAMCMVTRTEKDSYVAAFSDENVP 436
 QY 422 CPVTTDMTLQOVLAMASQIPAGGTDCLPMIWAQKNTNPADVFIYFTDNETPAGGVHPAI 481
 DB 437 CPVTTDMTLQOVLAMASQIPAGGTDCLPMIWAQKNTNPADVFIYFTDNETPAGGVHPAI 496
 QY 482 ALREYRKQNDIPAKLIVCGMTSNGFTIADPDDRGMLDMCGFDTGALDVIRNFTLDMI 538
 DB 497 ALREYRKQNDIPAKLIVCGMTSNGFTIADPDDRGMLDMCGFDTGALDVIRNFTLDMI 553

RESULT 6
 US-10-615-515-10
 Sequence 10, Application US/10615515
 Publication No. US20040132974A1
 GENERAL INFORMATION:
 APPLICANT: PAGAN, RICHARD, JOSEPH
 APPLICANT: GOTTERIDGE, ALEX
 APPLICANT: PHELPS, CHRISTOPHER BENJAMIN
 TITLE OF INVENTION: ADHESION MOLECULES
 FILE REFERENCE: 674575-2004
 CURRENT APPLICATION NUMBER: US/10/615,515
 CURRENT FILING DATE: 2003-07-08
 PRIOR APPLICATION NUMBER: PCT/GB02/00107
 PRIOR FILING DATE: 2002-01-11
 PRIOR APPLICATION NUMBER: GB 0100750.9
 PRIOR FILING DATE: 2001-01-11
 NUMBER OF SEQ ID NOS: 12
 SOFTWARE: PatentIn Ver. 3.2
 SEQ ID NO 10

```

; LENGTH: 537
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-615-515-10

Query Match          90.5%; Score 2522.5; DB 4; Length 537;
Best Local Similarity 89.8%; Pred. No. 2.3e-219;
Matches 483; Conservative 28; Mismatches 26; Indels 1; Gaps 1;

QY 1 MESSVNOMOPINERKQIANSODGYVQVTDNMRILHRLFCFSGEGTYYIKKQKGLLENAA 60
D 1 MEGSANOLOPLSEFTQVNVSEGGCWQVTDNQ-VRRFLCFSGEGTYYIKKQKGLLENAA 59
QY 61 LIRLIDGRGCEVIOEIKSFQSGRTTKQEPMLPALAICSCQSDISTKQAFKAVSEVCR 120
D 60 LIRLIDGRGCEVIOEIKSFQSGRTTKQEPMLPALAICSCQSDISTKQAFKAVSEVCR 119
QY 121 IPTHLFTFIQPKDKLKSMMCGMGRALRKAIADWYNEKGMALALAVTKYKQKNGSHK 180
D 120 IPTHLFTFIQPKDKLKSMMCGMGRALRKAIADWYNEKGMALALAVTKYKQKNGSHK 179
QY 181 DLRLSLHKPSSSEGIAIVTKYITGKMKVHELYEKALSVTEKLLKYLEAVEKVKTKD 240
D 180 DLRLSLHKPSSSEGIAIVTKYITGKMKVHELYEKALSVTEKLLKYLEAVEKVKTKD 239
QY 241 ELRVIHLIEHRILVREHLITNHLKSKEVWKLLOEMPLTALLRNLGKWTANSVLEPGNSE 300
D 240 ELRVIHLIEHRILVREHLITNHLKSKEVWKLLOEMPLTALLRNLGKWTANSVLEPGNSE 299
QY 301 VSLVCEKLCNEKLLKKARIPHPHILIALETYKTHGHLRGKLRPDEBILKALDAAFYKT 360
D 300 VSLVCEKLCNEKLLKKARIPHPHILIALETYKTHGHLRGKLRPDEBILKALDAAFYKT 359
QY 361 FKTYEPTGKRFLLAVDVASANNQVLSIINASTVAAACMVVTRTEKOSVVAFSDEMV 420
D 360 FKTYEPTGKRFLLAVDVASANNQVLSIINASTVAAACMVVTRTEKOSVVAFSDEMV 419
QY 421 PCPVTDMTLQOVLVMAISOIPAGGTDCLPMIWAOKNTPADVIVFTDNETFAGVHPA 480
D 420 PCPVTDMTLQOVLVMAISOIPAGGTDCLPMIWAOKNTPADVIVFTDNETFAGVHPA 479
QY 481 IALREYRKMDIPAKLIYCGMTSNGFTIADPDRGMLDMCGFDGALDVIRNFTLDM 538
D 480 VALREYRKMDIPAKLIYCGMTSNGFTIADPDRGMLDMCGFDGALDVIRNFTLDM 537

RESULT 7
US-10-615-515-11
; Sequence 11, Application US/10615515
; Publication No. US20040132974A1
; GENERAL INFORMATION:
; APPLICANT: PAGAN, RICHARD, JOSEPH
; APPLICANT: PHELPS, CHRISTOPHER BENJAMIN
; TITLE OF INVENTION: ADHESION MOLECULES
; FILE REFERENCE: 674575-2004
; CURRENT APPLICATION NUMBER: US/10/615, 515
; PRIOR FILING DATE: 2003-07-08
; PRIOR APPLICATION NUMBER: PCT/GB02/00107
; PRIOR FILING DATE: 2002-01-11
; PRIOR APPLICATION NUMBER: GB 0100750.9
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 11
; LENGTH: 538
; TYPE: PRT
; ORGANISM: Xenopus laevis
US-10-615-515-11

Query Match          81.4%; Score 2269; DB 4; Length 538;
Best Local Similarity 78.6%; Pred. No. 2.2e-196;
Matches 423; Conservative 59; Mismatches 56; Indels 0; Gaps 0;

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QY 1 MESSVNOMOPINERKQIANSODGYVQVTDNMRILHRLFCFSGEGTYYIKKQKGLLENAA 60
D 1 MEATMDOTPLNKKQVNSGCTVMOVSDNNRLRFLFCFSGEGTYYIKKQKGLLENAA 60
QY 61 LIRLIDGRGCEVIOEIKSFQSGRTTKQEPMLPALAICSCQSDISTKQAFKAVSEVCR 120
D 61 LIRLIDGRGCEVIOEIKSFQSGRTTKQEPMLPALAICSCQSDISTKQAFKAVSEVCR 120
QY 121 IPTHLFTFIQPKDKLKSMMCGMGRALRKAIADWYNEKGMALALAVTKYKQKNGSHK 180
D 121 IPTHLFTFIQPKDKLKSMMCGMGRALRKAIADWYNEKGMALALAVTKYKQKNGSHK 180
QY 181 DLRLSLHKPSSSEGIAIVTKYITGKMKVHELYEKALSVTEKLLKYLEAVEKVKTKD 240
D 181 DLRLSLHKPSSSEGIAIVTKYITGKMKVHELYEKALSVTEKLLKYLEAVEKVKTKD 240
QY 241 ELRVIHLIEHRILVREHLITNHLKSKEVWKLLOEMPLTALLRNLGKWTANSVLEPGNSE 300
D 241 ELRVIHLIEHRILVREHLITNHLKSKEVWKLLOEMPLTALLRNLGKWTANSVLEPGNSE 300
QY 301 VSLVCEKLCNEKLLKKARIPHPHILIALETYKTHGHLRGKLRPDEBILKALDAAFYKT 360
D 301 VSLVCEKLCNEKLLKKARIPHPHILIALETYKTHGHLRGKLRPDEBILKALDAAFYKT 360
QY 361 FKTYEPTGKRFLLAVDVASANNQVLSIINASTVAAACMVVTRTEKOSVVAFSDEMV 420
D 361 FKTYEPTGKRFLLAVDVASANNQVLSIINASTVAAACMVVTRTEKOSVVAFSDEMV 420
QY 421 PCPVTDMTLQOVLVMAISOIPAGGTDCLPMIWAOKNTPADVIVFTDNETFAGVHPA 480
D 421 PCPVTDMTLQOVLVMAISOIPAGGTDCLPMIWAOKNTPADVIVFTDNETFAGVHPA 480
QY 481 IALREYRKMDIPAKLIYCGMTSNGFTIADPDRGMLDMCGFDGALDVIRNFTLDM 538
D 481 TALQYERKMDIPAKLIYCGMTSNGFTIADPDRGMLDMCGFDGALDVIRNFTLDM 538

RESULT 8
US-10-615-515-12
; Sequence 12, Application US/10615515
; Publication No. US20040132974A1
; GENERAL INFORMATION:
; APPLICANT: PAGAN, RICHARD, JOSEPH
; APPLICANT: PHELPS, CHRISTOPHER BENJAMIN
; TITLE OF INVENTION: ADHESION MOLECULES
; FILE REFERENCE: 674575-2004
; CURRENT APPLICATION NUMBER: US/10/615, 515
; PRIOR FILING DATE: 2003-07-08
; PRIOR APPLICATION NUMBER: PCT/GB02/00107
; PRIOR FILING DATE: 2002-01-11
; PRIOR APPLICATION NUMBER: GB 0100750.9
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 12
; LENGTH: 643
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-615-515-12

Query Match          36.3%; Score 1011; DB 4; Length 643;
Best Local Similarity 36.3%; Pred. No. 3.1e-82;
Matches 215; Conservative 111; Mismatches 204; Indels 62; Gaps 9;

QY 7 QMOPINERKQIANSODGYVQVTDNMRILHRLFCFSGEGTYYIKKQKGLLENAAIRLIE 66
D 54 QMEKYKQGVENNAAGVFPVSDTQVRRFLILGSDKSHQSEKTIIDNAQNIKITE 113
QY 67 DGRGCEVIOEIKSFQSGRTTKQEPMLPALAICSCQSDISTKQ----- 109
D 114 QGNHMYLKEIALINAEINRNPKNAMIFTLAICARISTHDTTKTECPMLNAYS DYIRAL 173

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110 --AAEKAASVCRIPHTLFTPIQFKDLKESNKG-----MGRALRKALADYNEKG 161
 174 HDSALDLIPVCRFTPLFFBFDVYCOTISESTKAGAKSSTGWSMNAISKWTTTKT 233
 162 MALAAVTKYQORNGMSHKDLRLSH---LKPSSGLA-----IYKITYKG----- 205
 234 EKLMLLTKYQOREGMSHRDLFRLAHPNLMDSRSHQSEDLREBQLFRPAVGDLVRK 293
 206 -----WKEVHELKELASV-----ETKLLKYLEAVKVKRTODELEVIHLI 248
 294 RKMVEEVAEVEKMKALKLPYEBOLIKEGBALNLPYAKLKEGSEEVYVAI 353
 249 EEBRLVREHLITNHLKSEVWKALIQ-EMPTALLRNIGKMTANSVLEPNSSEVLCVK 307
 354 KKGIVRHLPTTSLNSKLWVETLFPDVGMPMTAMIRNLAKTIVGALD--EKRVNIVR 411
 308 LCNELKAKKARIHPHILIALETTYKTHGRLKMKRPDEILKALDAFYTKTEVPT 367
 412 LTDOELRERSRHPINLTPARAIVAQGRGDKSLTWEPQKICDLEAGFYAFVNAAPT 471
 368 GKRPLAVDVASAMQVYGSILNASVAAACMVVTRTEKDSYVAFSDEWPCPTTD 427
 472 GRYCLADVSGSMTSRVSSPLSCREAAITGMSLINLHAEAVRCVAPCDKLTLPFKD 531
 428 MTLQOVLAMASQIPAGTDCSLPMIAOKTNPADVFTVFTDNETFAGGVHAPALREXR 487
 532 WKIGVNVYNNLDPGRDTCGLPMTWATENNLLKPVFIITYDNDTWAGIHFPBAIKKR 591
 488 KKMID-PAKLIYCGMTSNGFTIADPDDRGMLDMCGEPTGALDVIIRNFTLDM 538
 592 EASGHDHAKVIVMAQAYDYSIADPSDAGMLDITGDSAVPQIVHFEVTKGI 643

RESULT 9
 US-11-097-143-5949
 / Sequence 5949, Application US/11097143
 / Publication No. US20050208558A1
 / GENERAL INFORMATION:
 / APPLICANT: Venter, J. Craig
 / APPLICANT: et al.
 / TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
 / TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
 / FILE REFERENCE: CLO000728
 / CURRENT APPLICATION NUMBER: US/11/097,143
 / CURRENT FILING DATE: 2005-04-04
 / PRIOR APPLICATION NUMBER: 60/157,832
 / PRIOR FILING DATE: 1999-10-05
 / PRIOR APPLICATION NUMBER: 60/160,191
 / PRIOR FILING DATE: 1999-10-19
 / PRIOR APPLICATION NUMBER: 60/161,932
 / PRIOR FILING DATE: 1999-10-28
 / PRIOR APPLICATION NUMBER: 60/164,769
 / PRIOR FILING DATE: 1999-11-12
 / PRIOR APPLICATION NUMBER: 60/173,383
 / PRIOR FILING DATE: 1999-12-28
 / PRIOR APPLICATION NUMBER: 60/175,693
 / PRIOR FILING DATE: 2000-01-12
 / PRIOR APPLICATION NUMBER: 60/184,831
 / PRIOR FILING DATE: 2000-02-24
 / PRIOR APPLICATION NUMBER: 60/191,637
 / PRIOR FILING DATE: 2000-03-23
 / NUMBER OF SEQ ID NOS: 43008
 / SOFTWARE: PASTESEQ for Windows Version 4.0
 / SEQ ID NO: 5949
 / LENGTH: 641
 / TYPE: PR
 / ORGANISM: DROSOPHILA
 / US-11-097-143-5949

Query Match 6.7%; Score 185.5; DB 6; Length 641;
 Best Local Similarity 19.5%; Pred. No. 2.1e-07;

Matches 123; Conservative 108; Mismatches 242; Indels 159; Gaps 28;
 1 MESSVNOQPIANE---KQIANSQOG-YVQYTDNMRLLHRFLCPSS-BGGTYIIEQKGL 55
 64 MEKASISQPKDPPSPKDEPNQSGTAISTIPALDKARFCFISTDEPVTTPLADLV 123
 56 EN-----AEALIRLIEDPGEVIOEIKSF-----SQGRFTKQBPMLFALAIQSCSDI 105
 124 ENNPAASLKELCQVSED---ELVECLISVUGSEPNQPRPRPEBLLIILAVFTTCDE 179
 106 STKQAAFAVSEVCRIPHTLFTPIQFKDLKESN-KCGMGRALRKALADYNEKGAL 164
 180 KKRNAVRRPFDLTSSDILLFPQVYKQGLERKTPFRFTRKAVIANVYGT-K-SIDR 238
 165 ALAVTKYQORNG-MSKDLRLSHKSS--EGLAIVKITYTKGKVEH-----L 212
 239 LHFWSIGDGNRWAHRDLRLHFRHANFLPEIILALRLSSSPKELSQWPDFTPLTS 298
 213 YKELASVETKELKYLE-AVEKVKRTODELEVI--HLIEEBRLVREHLITNHLKSEV 269
 299 FRETBGVAKRLTDPQALSIYKLSLSWEHVPFILHDPRLA--HFLIPHS-----Y 352
 270 KALIQEMPTALLRNIGKMTANSVLEPNSSEVLCVKLCNEKLLKARIPHFILIALE 329
 353 EQLQKWRRLRL-----NSRVPRPAEQLLDKKCKAKSNVPPVRLLE-- 395
 330 TYKTHGRLKMKRPDEILKAL-----DAAFYK-----TFK 362
 396 -----DMRLKPKVYNQVLPSLKNKNTFKFOCATTSPOKASFLHSYVEISFG 445
 353 TVEPTGKFLAVDVASAMQVYGSILNAS-----TVAAACMVVTRTEKDSYVAF 415
 446 LNKALGRR---LHITTLLEQAVYLGKYLISGPPRSIKYLDALVALFGYFRSPKRYVERW 501
 416 SD---EMVPCPVYTDNTLQOVLAMASQIPAGTDCSLPMIAOKTNT----- 459
 502 HDRSGKLALPWTNMSVSE-----AKTCB-----NQKNTPHNRSPVFTIDLR 546
 547 PRALDMQNTFDFVFLVPG---AARGNPENNSKCLALMLDKYRKRSNAKIVMSLQ 603
 502 TSNGFTIADPDDRGMLDMCGEPTGALDVIIRNF 533
 604 RQSMIYSSGRNENLELCSDLKHTPRLINAF 635

RESULT 10
 US-09-843-676-52
 / Sequence 52, Application US/09843676
 / Patent No. US20020164786A1
 / GENERAL INFORMATION:
 / APPLICANT: Cech, Thomas R.
 / Lingner, Joachim
 / Nakamura, Toru
 / Chapman, Karen B.
 / Morin, Gregg B.
 / Harley, Calvin
 / Andrews, William H.
 / TITLE OF INVENTION: No. US20020164786A1el Telomerase
 / NUMBER OF SEQUENCES: 225
 / CORRESPONDENCE ADDRESS:
 / ADDRESS: Townsend and Townsend and Crew LLP
 / STREET: Two Embarcadero Center, 8th Floor
 / CITY: San Francisco
 / STATE: California
 / COUNTRY: United States of America
 / ZIP: 94111
 / COMPUTER READABLE FORM:
 / MEDIUM TYPE: Floppy disk
 / COMPUTER: IBM PC compatible
 / OPERATING SYSTEM: PC-DOS/MS-DOS
 / SOFTWARE: PatentIn Release #1.0, Version #1.30

```

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/843,676
FILING DATE: 26-Apr-2001
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 699 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 52:
US-09-843-676-52

Query Match          6.5%; Score 180.5; DB 3; Length 699;
Best Local Similarity 20.7%; Pred. No. 6.7e-07;
Matches 115; Conservative 100; Mismatches 191; Indels 149; Gaps 29;

QY 102 CSDISTQAAPKAVSEVCRIPTHLFTPIQFKDLKESKCGMGRALRKALADYNYNEKG 161
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 175 CTESQKKTWFRYLS-----VTNKQKMDQTKKKRKENILTL--QAIKESDKSKRETD 227
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 162 M-----ALALAVTK--YKORNGSHKDLRLSHLK-PSSEGLATVTKYITGKMEVH 210
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 228 IMNVEDAIKALKPVMKKIARQUNMK-----KHMKAPKIPNSTLESKTLT-----FK 275
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 211 ELYEKALSVETETKLKYLBAVEKVKRTKDELEVH-----LIEHRILVREHLLT 260
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 276 DLIFCHISPEKEVYKILG--KYPKTEBEYKAFQDSASAPNPBLAGRMKIEISKI 333
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 261 --NHLKSK---EYWKALL--QEMPTALLRNIGMTANSVLEPQNSBV--SLVCEKLCN 310
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 334 WENELSAKGNTAEVWDLNLISSNQLPYVAMLNLT-----SNILKAGVSDTTHSIYINKICE 388
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 311 EKLAKKARIHPHILIALETY-----KTGHGLRGKL-----KMRPDE 347
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 389 PKAVENSKMPFLOFESALBAVNEAVTKGFKAKKERNMNLKQILBAVKEVEKTEDEKKDM 448
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 348 EILVALDAAPKTFKTEVPTGKRL-----LAV-----DVGSAMNQR 384
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 449 ELBOEBEERF---VKVNEGIGKOYINSHELAKIAVKNQDEIKHTAIFSDVGSMSSTS 505
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 385 VLGSILNASTVAAAM-----CMVVTETEKDSYVV--AFSDENVPCFVTDM-----428
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 506 MSGGAKKGVSRVTCLECALVGLWVKQRCESFYIFSPSSQCKCYLAVDLPCODELRP 565
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 429 TLQOVLAMSGQIPAGGTCSLPMI--WAQKNTTPADVIVFTDNETFG-----GNHP 479
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 566 SMOQLLQKGLT--GGGTDFPYECIDEWL--KQKTHVDNVLIIIDMWIAAGYSDINVRGSSI 623
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 480 AIALREYKKNDDIPAKLIVCGWTSNG--FTIADP--DGRGMLDMCGFDYDAL-----527
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 624 VNSIKKIDENVNPKIPIAVDLLEGYCKLNLGDEPENNNYIKIRGMSDSILKFIKAKGGS 683
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 528 ----DVINFTLDMT 538
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 684 ANMVEVINKPFLQKI 698

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```

RESULT 11
US-09-766-253-52
; Sequence 52, Application US/09766253
; Publication No. US20020187471A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
;           Lingner, Joachim
;           Nakamura, Toru
;           Chapman, Karen B.
;           Morin, Gregg B.
;           Harley, Calvin
;           Andrews, William H.
; TITLE OF INVENTION: No. US20020187471A1el Telomerase
; NUMBER OF SEQUENCES: 171
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/766,253
; FILING DATE: 19-Jan-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/846,017
; FILING DATE: 1997-04-25
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002920US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 699 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 52:
US-09-766-253-52

Query Match          6.5%; Score 180.5; DB 3; Length 699;
Best Local Similarity 20.7%; Pred. No. 6.7e-07;
Matches 115; Conservative 100; Mismatches 191; Indels 149; Gaps 29;

QY 102 CSDISTQAAPKAVSEVCRIPTHLFTPIQFKDLKESKCGMGRALRKALADYNYNEKG 161
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 175 CTESQKKTWFRYLS-----VTNKQKMDQTKKKRKENILTL--QAIKESDKSKRETD 227
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 162 M-----ALALAVTK--YKORNGSHKDLRLSHLK-PSSEGLATVTKYITGKMEVH 210
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 228 IMNVEDAIKALKPVMKKIARQUNMK-----KHMKAPKIPNSTLESKTLT-----FK 275
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 211 ELYEKALSVETETKLKYLBAVEKVKRTKDELEVH-----LIEHRILVREHLLT 260
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 276 DLIFCHISPEKEVYKILG--KYPKTEBEYKAFQDSASAPNPBLAGRMKIEISKI 333
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 261 --NHLKSK---EYWKALL--QEMPTALLRNIGMTANSVLEPQNSBV--SLVCEKLCN 310
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 334 WENELSAKGNTAEVWDLNLISSNQLPYVAMLNLT-----SNILKAGVSDTTHSIYINKICE 388

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QY 311 EKLKKARIHPHIIIALETY-----KTGHGIRGL-----KMRPDE 347
D 389 PKAVNSKMPFLQFSAIEAVNEAVTKGPKAKKRENNMLKQIIEAVKEVEKTEDEKKDM 448
QY 348 EILKALDAAFKPTKPTVEPTGKRL-----LAV-----DVSASMNQR 384
D 449 ELEQTEEBGF--VAVNEGIGKQYINSIELAKIAVNKNLDEIKGHTAIFSDVSGSMSTS 505
QY 385 VIGSILNASTYAAAM-----CMVVTREKDSYVV--AFSDENVPCEVTIDM-----428
D 506 MSGAKKYGSRVTCIECALVIGLAWKORCEKSSFYIFSSPQCNKCYLIEVDLPDDELRLP 565
QY 429 TLQOVLAMMSOI PAGTDCSLPMI--WAQKTNPADVPFIVFTDNETPAG-----GVHP 479
D 566 SMQKLOEKKGL-GGGTDFPYECIDEMT-KNKTIVDNIVILSDMMIABGYSDINVRGSSI 623
QY 480 AIALREYRKNDIPAKLIVCGMTSNG--FTIADP--DDRGMLDMCGPDTGAL-----527
D 624 VNSIKKYDEVNPNIKIFAVDLBGYGKCLNLGDBERNENNYIKIFGMSDSLKFISAKQGG 683
QY 528 ----DVIRNFTLDMI 538
D 684 ANMVEVIKNFALQKI 698

RESULT 12
US-09-438-486-52
Sequence 52, Application US/09438486
Publication No. US20030009019A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin H.
TITLE OF INVENTION: No. US20030009019A1el Telomerase
NUMBER OF SEQUENCES: 223
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/438,486
FILING DATE: 12-NOV-1999
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:

```

```

NAME: Apple, RandoJph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002931US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 699 amino acids
STRANDEDNESS:
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-438-486-52

Query Match 6.5%; Score 180.5; DB 3; Length 699;
Best Local Similarity 20.7%; Pred. No. 6.7e-07;
Matches 115; Conservative 100; Mismatches 191; Indels 149; Gaps 29;

QY 102 CSDISTKQAAFKAVSEVCRIPTHLFTFIQPKKDLKESMKCGMGRALKATADWYNEKGG 161
D 175 CTESQKKTTFRRYLS-----VTKQKMDQTKKKRKENLITKL--QAIKSEBKSREFTGD 227
QY 162 M-----ALALAVTK--YKQRNGSMHKLRLRSLHK-PSSEGLAIVTKYITKGMKEVH 210
D 228 IANVEDAIKALKPAMKKAIAKQNAK-----KEMKAPKIPNGLSKYLT-----FK 275
QY 211 ELYEKALSVETEKLLKYLEAVEKYKRTKDELEVIH-----LIEHRILVNEHLIT 260
D 276 DLIKFCHISEPKERYKILG--KKYPKTEBEYKAFGDSASAPFNPBLAGKMKIEISKI 333
QY 261 --NHLKSK-----EYWKALL--QEMPLTALLNLTGKMTANSVLEPNSSEV--SLYCEKLCN 310
D 334 WENELSAAGNTAEVADNLISSNQLPYMMLRNL-----SNLIKAGVSDTTHSIVINKICE 388
QY 311 EKLKKARIHPHIIIALETY-----KTGHGIRGL-----KMRPDE 347
D 389 PKAVNSKMPFLQFSAIEAVNEAVTKGPKAKKRENNMLKQIIEAVKEVEKTEDEKKDM 448
QY 348 EILKALDAAFKPTKPTVEPTGKRL-----LAV-----DVSASMNQR 384
D 449 ELEQTEEBGF--VAVNEGIGKQYINSIELAKIAVNKNLDEIKGHTAIFSDVSGSMSTS 505
QY 385 VIGSILNASTYAAAM-----CMVVTREKDSYVV--AFSDENVPCEVTIDM-----428
D 506 MSGAKKYGSRVTCIECALVIGLAWKORCEKSSFYIFSSPQCNKCYLIEVDLPDDELRLP 565
QY 429 TLQOVLAMMSOI PAGTDCSLPMI--WAQKTNPADVPFIVFTDNETPAG-----GVHP 479
D 566 SMQKLOEKKGL-GGGTDFPYECIDEMT-KNKTIVDNIVILSDMMIABGYSDINVRGSSI 623
QY 480 AIALREYRKNDIPAKLIVCGMTSNG--FTIADP--DDRGMLDMCGPDTGAL-----527
D 624 VNSIKKYDEVNPNIKIFAVDLBGYGKCLNLGDBERNENNYIKIFGMSDSLKFISAKQGG 683
QY 528 ----DVIRNFTLDMI 538
D 684 ANMVEVIKNFALQKI 698

RESULT 13
US-10-053-758-52
Sequence 52, Application US/10053758
Publication No. US20030032075A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin H.
TITLE OF INVENTION: No. US20030032075A1el Telomerase

```

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NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/053,758
FILING DATE: 18-Jan-2002
CLASSIFICATION: 536

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996

ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 699 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 52:
US-10-053-758-52

Query Match 6.5%; Score 180.5; DB 4; Length 699;
Best Local Similarity 20.7%; Pred. No. 6.7e-07;
Matches 115; Conservative 100; Mismatches 191; Indels 149; Gaps 29

QY 102 CSDISTKQAAKAAVSEVCRIPHTLPTFLOFKKDLKESKCGMGGRALRKALIDWYNEKG 161
Db 175 CTEGQRKKTMYRYS-----VTNRQKMQQTQKKRKENLITLK--QAKSEDSKRETD 227
QY 162 M-----ALAAVTK--YKORNGSHKDLRLSHLK-PSEEGAIYVTKYITTKGKVEH 210
Db 228 IMNVEDAIKALKPAVMKKIARKQNMK-----KMKAPKIPNSTLBSKYLT-----PK 275
QY 211 ELVYEKALSVTEKLYKYLEAVEXYKRTQDELEVH-----LIEHNLVREHLLT 260
Db 276 DLIRFCHISPEKERYKILG--KTKPKTEEEYKAAFPQDSASAPRPDELAKMKKIEIST 333
QY 261 --NHLKSK---EWKALL--QEMFLTALRLNGKGTANSVLEPGNSEV--SLVCEKLCN 310
Db 334 WENLSAGNTAEAVVDNLISNQGLPYMAWLRNL-----SNLKAGVSDTTHIVINKICE 388
QY 311 EKLKKAIRHPHILIALETY-----KTHGGLRGKL-----KKRPDE 347
Db 389 PKAVENSKTFLOPFSALAEVAVNEAVTGFKAKKRNNMLKQIEAVKEVVEKTEDEKCM 448
QY 348 ELWALDAAPKTFPTVEPTGRPL-----LAV-----DVSAENQR 384
Db 449 ELQTEBGEF--VKNVEIGIQYINSLTALAKIANKRLDEIKGHTALFSDVSGSMST 505

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QY 385 YIGSLINASTVAAA-----CWVTEKDSYV--AFSDMVPPTTDM-----448
Db 506 MSGGAKKGVSVTTCLECLVLGLMVKQRCESYFITS9BSQCNKCYLAVLDLPGDELRP 565
QY 429 TLQOVLWMSQIPAGTDCSLPMI--WAQKNTNPADVFIYFTDNETFAG-----GVHP 479
Db 566 SMQKLLQEGKRL--GGGTDFPEYCEIDEMT--KKKTHVDNIVLISDMMIAEGSDINVRSS1 623
QY 480 AIALREYRKMDIIPAKLVICMTSNG--FTIADP--DDRGLMDGSPDTGL-----527
Db 624 VNSIKKYYKQEVNPNIKIPAVDLEGGKCLNLGDEFENENYIKIYGMDSILKFI5AKQGG 683
QY 528 ----DYIRNFTLDMI 538
Db 684 ANNVEYIKYFALQKI 698

RESULT 14
US-10-054-295-52
; Sequence 52, Application US/10054295
; Publication No. US20030044953A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: No. US20030044953A1el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/054,295
FILING DATE: 18-Jan-2002
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/854,050
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 013389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 699 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 52:
US-10-054-295-52

```

Query Match 6.5%; Score 180.5; DB 4; Length 699;
 Best Local Similarity 20.7%; Pred. No. 6.7e-07;
 Matches 115; Conservative 100; Mismatches 191; Indels 149; Gaps 29;

102 CSDISTKQAFKAVSEVCRIPHTLFTPIQFKDLKESKCGMGMGALKALADWYNEKGG 161
 175 CTESQKKTMTFRYLS-----VTNKKQMDQTKKRRKENLITKL--QAIKSEBKSRETEGD 227
 162 M-----ALALAVTK--YKQRNGMSHKDLRLSLHK--PSSEGLAVTKYITKGMKEVH 210
 228 INNVEDAIKALKPAMKTIARQNMK-----KMKAPKIPNSTLSKYLT-----FK 275
 211 BLYEKALSVETEKLLKYLEAVEKRYKTDELEVH-----LIEHRLVBEHLIT 260
 276 DLKFCHESEPEREYKILG--KTKPKTEEBEYKAFGDSASAPFNPBLAGKMKIEISKI 333
 261 --NHLKSK---EYWKALL--QEMPLTALLRNIGKMTANSVLEPGNSEV--SLVCEKLCN 310
 334 WENELSAKGNLTAEVMDNLSSNQLPYMAMLRNL-----SNILKAGVSDTTHSIVINKICE 388
 311 EKLKKARIHPHILIALETY-----KTGHGLRGKL-----KMRPDE 347
 389 PRAVENSXMFLOPFSALAEAVNEAVTKGPKAKKRENNMLKGQIBAVKEVEKTDDEKDM 448
 348 EILKALDAAFYKTFKVEPTGKFL--LAV-----DVSASMNOR 384
 449 ELEQTEBEGF--VKVNEGIGKQYINSIELAKIANKNLDEIKGHTALFSDVSGSMSTS 505
 385 VIGSLINSTVAAAM-----CMVTRTEKDSYVV--AFSDMVPCEVTTDM----- 428
 506 MSGAKKGTGVSRTCTECALVLGLMVKORCEKSFYFSSPSQCNKYLEVLDLPGDELRLP 565
 429 TIQOVLAMMSQIPAGTDCSLPMI--WAQKNTVPADVFLVFITDNETFAG-----GVHP 479
 566 SMQKLOEKGKL--GGTDPPEYCIDBWT--KNTTHVNIIVILSDMIAEGYSIDINRGSSI 623
 480 AIALREYRKMDIPAKLIVCGMTSNG--FTIADP--DDRGMIDMCGFTGAL----- 527
 624 VNSIKKYKQEVNPNIKIPAVDLEGYCKLNLGDEFENNNYIKIFGMSDSILKFIKAKOG 683
 528 ---DVIRNFTLDMI 538
 684 ANNVEVIKNFALOKI 698

RESULT 15

US-10-054-611-52

Sequence 52, Application US/10054611

Publication No. US20030059787A1

GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.

lingnet, Joachim

Nakamura, Toru

Chapman, Karen B.

Morin, Gregg B.

Harley, Calvin

Andrews, William H.

TITLE OF INVENTION: No. US20030059787A1el Telomerase

NUMBER OF SEQUENCES: 225

CORRESPONDENCE ADDRESS:

ADDRESSER: Townsend and Crew LLP

STREET: Two Embarcadero Center, 8th Floor

CITY: San Francisco

STATE: California

COUNTRY: United States of America

ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/054,611

FILING DATE: 18-Jan-2002

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/854,050

FILING DATE: <Unknown>

APPLICATION NUMBER: US 08/846,017

FILING DATE: 25-APR-1997

APPLICATION NUMBER: US 08/844,419

FILING DATE: 18-APR-1997

APPLICATION NUMBER: US 08/724,643

FILING DATE: 01-OCT-1996

ATTORNEY/AGENT INFORMATION:

NAME: Apple, Randolph T.

REGISTRATION NUMBER: 36,429

REFERENCE/DOCKET NUMBER: 015389-002930US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 52:

SEQUENCE CHARACTERISTICS:

LENGTH: 699 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 52:

US-10-054-611-52

Query Match 6.5%; Score 180.5; DB 4; Length 699;
 Best Local Similarity 20.7%; Pred. No. 6.7e-07;
 Matches 115; Conservative 100; Mismatches 191; Indels 149; Gaps 29;

102 CSDISTKQAFKAVSEVCRIPHTLFTPIQFKDLKESKCGMGMGALKALADWYNEKGG 161
 175 CTESQKKTMTFRYLS-----VTNKKQMDQTKKRRKENLITKL--QAIKSEBKSRETEGD 227
 162 M-----ALALAVTK--YKQRNGMSHKDLRLSLHK--PSSEGLAVTKYITKGMKEVH 210
 228 INNVEDAIKALKPAMKTIARQNMK-----KMKAPKIPNSTLSKYLT-----FK 275
 211 BLYEKALSVETEKLLKYLEAVEKRYKTDELEVH-----LIEHRLVBEHLIT 260
 276 DLKFCHESEPEREYKILG--KTKPKTEEBEYKAFGDSASAPFNPBLAGKMKIEISKI 333
 261 --NHLKSK---EYWKALL--QEMPLTALLRNIGKMTANSVLEPGNSEV--SLVCEKLCN 310
 334 WENELSAKGNLTAEVMDNLSSNQLPYMAMLRNL-----SNILKAGVSDTTHSIVINKICE 388
 311 EKLKKARIHPHILIALETY-----KTGHGLRGKL-----KMRPDE 347
 389 PRAVENSXMFLOPFSALAEAVNEAVTKGPKAKKRENNMLKGQIBAVKEVEKTDDEKDM 448
 348 EILKALDAAFYKTFKVEPTGKFL--LAV-----DVSASMNOR 384
 449 ELEQTEBEGF--VKVNEGIGKQYINSIELAKIANKNLDEIKGHTALFSDVSGSMSTS 505
 429 TIQOVLAMMSQIPAGTDCSLPMI--WAQKNTVPADVFLVFITDNETFAG-----GVHP 479
 566 SMQKLOEKGKL--GGTDPPEYCIDBWT--KNTTHVNIIVILSDMIAEGYSIDINRGSSI 623
 480 AIALREYRKMDIPAKLIVCGMTSNG--FTIADP--DDRGMIDMCGFTGAL----- 527
 624 VNSIKKYKQEVNPNIKIPAVDLEGYCKLNLGDEFENNNYIKIFGMSDSILKFIKAKOG 683
 528 ---DVIRNFTLDMI 538
 684 ANNVEVIKNFALOKI 698

Fri Jan 13 11:44:12 2006

us-10-615-515-6.rapbm

Page 10

Search completed: January 13, 2006, 11:21:45
Job time : 118 secs

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Db      65 SHAVSLHGNKKQ-----NIEGAFGLSLAKQHLANN-NELKILRADTF-PGIENTL 115
      196 AI-----VTKYITGKMEVHELYKEKALSVETEKLLKYIEAVEKVKRTKODELEVIHLIE 249
      116 EYLQADVYLKYEIRG--AFNKLHKLKVL-ILNDNLISFL-----152
Qy      250 EHLVREHLLTNHLKSEKVEWALLQEMPLTALLNLIGMTANSYLE-PGNSEVSLVCEKL 308
      153 PDNIFRPSLTL-HL--DIRGNRIQKLPYIGVLHEIRGVELQJEDPMWNCSDLLPLKA 208
Qy      309 CNEKILKKARIHPHILIALETYKTHGHLRGKLMKRPDEEILKALDAFYKTFKTEVPTG 368
      209 WLENN-----PYNITIGEAICETPSDLVGRLL-----LKETN 239
Qy      369 KRFLIADVASAMNQRVLG-----SIINASTVAAAMCMVTRTEKDSYVAFPSBMY 420
      240 KOELCPMGTSDFVRLILPSPQLENGYYTPNGHTTQTSIHLVTKRPKTPNPSKISG-IV 298
Qy      421 PCPVTDMTLQOVLAMASQIPAGGTDCLPMIMAKTNPADVPIVFTDNETFAGVHFA 480
      299 AGKALSRNLSQIVSYQTRVPP-LTPCPAPCF-C-KTH-PSDGLSVNCOEKNIQSMSEL 354
Qy      481 IALREYRKMDIPAKLIVCGMTSNGFTIADPDDRGMLDMCGFDTGAL-----DVI 530
      355 IPRKLNKXKLVH-----NGNSIKQVDVSDPTDFGGLDLHLHGSNQITVIKGDVF 403
Qy      531 RNFT 534
      404 HNLT 407

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RESULT 2

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US-10-453-372-1206
/ Sequence 1206, Application US/10453372
/ Publication No. US2006003233A1
/ GENERAL INFORMATION:
/ APPLICANT: Alabrook, et al.
/ TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
/ FILE REFERENCE: 21402-589 A
/ CURRENT APPLICATION NUMBER: US/10/453,372
/ PRIOR FILING DATE: 2003-06-03
/ PRIOR APPLICATION NUMBER: 09/789390
/ PRIOR FILING DATE: 2001-02-23
/ PRIOR APPLICATION NUMBER: 60/185967
/ PRIOR FILING DATE: 2000-03-01
/ PRIOR APPLICATION NUMBER: 09/823187
/ PRIOR FILING DATE: 2001-03-29
/ PRIOR APPLICATION NUMBER: 60/195792
/ PRIOR FILING DATE: 2000-03-10
/ PRIOR APPLICATION NUMBER: 09/839446
/ PRIOR FILING DATE: 2001-03-19
/ PRIOR APPLICATION NUMBER: 60/199476
/ PRIOR FILING DATE: 2000-03-25
/ PRIOR APPLICATION NUMBER: 09/863776
/ PRIOR FILING DATE: 2001-05-23
/ PRIOR APPLICATION NUMBER: 60/208263
/ PRIOR FILING DATE: 2000-05-31
/ PRIOR APPLICATION NUMBER: 09/939398
/ PRIOR FILING DATE: 2001-08-24
/ PRIOR APPLICATION NUMBER: 60/227800
/ PRIOR FILING DATE: 2000-08-25
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 1609
/ SOFTWARE: Curaseqlist version 0.1
/ SEQ ID NO 1206
/ LENGTH: 600
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-453-372-1206

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Query Match 3.5%; Score 98.5; DB 6; Length 600;
Best Local Similarity 19.0%; Pred. No. 1.7;

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Matches 92; Conservative 76; Mismatches 191; Indels 125; Gaps 21;
Qy      95 ALAICSCSDISIRKQAFKAVSEV-----CPIPTLFFPIQPK-----DL 135
      7 SVEICNVSCSVSENVLYVNCESKVSYPNQLKPEMSNFHLNFQNNPLAILYPTNLNF 66
      136 KESKICGMGRALRKALIDVYNEKGWALALAVTKYKQRNGWSHKDLLRLSHLKPSSGL 195
      67 SHAVSLHGNKKQ-----NIEGAFGLSLAKQHLANN-NELKILRADTF-PGIENTL 117
Qy      196 AI-----VTKYITGKMEVHELYKEKALSVETEKLLKYIEAVEKVKRTKODELEVIHLIE 249
      118 EYLQADVYLKYEIRG--AFNKLHKLKVL-ILNDNLISFL-----154
Qy      250 EHLVREHLLTNHLKSEKVEWALLQEMPLTALLNLIGMTANSYLE-PGNSEVSLVCEKL 308
      155 PDNIFRPSLTL-HL--DIRGNRIQKLPYIGVLHEIRGVELQJEDPMWNCSDLLPLKA 210
Qy      309 CNEKILKKARIHPHILIALETYKTHGHLRGKLMKRPDEEILKALDAFYKTFKTEVPTG 368
      211 WLENN-----PYNITIGEAICETPSDLVGRLL-----LKETN 241
Qy      369 KRFLIADVASAMNQRVLG-----SIINASTVAAAMCMVTRTEKDSYVAFPSBMY 420
      242 KOELCPMGTSDFVRLILPSPQLENGYYTPNGHTTQTSIHLVTKRPKTPNPSKISG-IV 300
Qy      421 PCPVTDMTLQOVLAMASQIPAGGTDCLPMIMAKTNPADVPIVFTDNETFAGVHFA 480
      301 AGKALSRNLSQIVSYQTRVPP-LTPCPAPCF-C-KTH-PSDGLSVNCOEKNIQSMSEL 356
Qy      481 IALREYRKMDIPAKLIVCGMTSNGFTIADPDDRGMLDMCGFDTGAL-----DVI 530
      357 IPRKLNKXKLVH-----NGNSIKQVDVSDPTDFGGLDLHLHGSNQITVIKGDVF 405
Qy      531 RNFT 534
      406 HNLT 409

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RESULT 3

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US-10-821-234-975
/ Sequence 975, Application US/10821234
/ Publication No. US2005025511A1
/ GENERAL INFORMATION:
/ APPLICANT: Labach, Ivan
/ APPLICANT: Steache-Crain, Birgitte
/ APPLICANT: Andarman, Susan
/ TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
/ FILE REFERENCE: 821A
/ CURRENT APPLICATION NUMBER: US/10/821,234
/ PRIOR FILING DATE: 2004-04-07
/ PRIOR APPLICATION NUMBER: US 60/462,047
/ NUMBER OF SEQ ID NOS: 1704
/ SOFTWARE: PL_SEQ_genes Version 1.0
/ SEQ ID NO 975
/ LENGTH: 989
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-821-234-975

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Query Match 3.5%; Score 98.5; DB 6; Length 989;
Best Local Similarity 20.2%; Pred. No. 3.4;
Matches 67; Conservative 75; Mismatches 114; Indels 75; Gaps 16;

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Qy      49 KEQKLGLENAL-----IRLIED-----GRGCEVIOEI--KSPSQ 82
      513 KQKLGIVSPESMNYSHFHELRATVEEINVTKQDLQNALSESRNNEKVALEBKLYER 572
      83 EGRITKQPM-LFALAIICSCSDIS--TKQAF-----KAVSVCKRIPTHLFFPIQPK- 132
      573 EKGTVIKPVEYEMKSSYCSYIENMKERKAFLEFKYQEAQOEIIMKDKTLKSGQMTQEA 632

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QY 133 ----KDLKESN-----KCGMGRALRAIDWNEKCGMALALAVTKYKORNGKSH 179
 DB 633 SDEADMEKANRMIDELNKOVELSOLYKEAQALEBDRYRKRSLEDYTAIYHKA--EH 690
 QY 180 KDLRLSLHK--PSEGLATYTKYTKMKWKEVHEL-----YKEKALSVETBKLLKYLEA 231
 DB 691 EKMQLTWSRPAKEDALSEKSOYSKVLNBLTOLKOLVDOKENSYSI-----TERHQV 745
 QY 232 VEKVRRTKDELEVIHLIEHRLVREHLITNHLKSKVWKLLOEMP--LTALLRLNGHRT 289
 DB 746 ITTIRTAKEHE-----EKISNKEHLASKEVEVAKLEKOLLEKAAWTDAMVPRSSYEV 800
 QY 290 ANSVLEPNSSEVSLVCEKLCNEKLLKARIRH 320
 DB 801 LQSSLE---SEVSVLASKL--KESVKEKEKVH 827

 RESULT 4
 US-11-124-368A-214
 ; Sequence 214, Application US/11124368A
 ; Publication No. US20050287559A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Michele Cargill
 ; APPLICANT: James J. Devlin
 ; APPLICANT: May Luke
 ; TITLE OF INVENTION: Genetic Polymorphisms Associated with
 ; TITLE OF INVENTION: Vascular Diseases, Methods of Detection and Uses Thereof
 ; FILE REFERENCE: CLO01524
 ; CURRENT APPLICATION NUMBER: US/11/124,368A
 ; CURRENT FILING DATE: 2005-05-09
 ; PRIOR APPLICATION NUMBER: US 60/568,845
 ; PRIOR FILING DATE: 2004-05-07
 ; PRIOR APPLICATION NUMBER: US 60/625,936
 ; PRIOR FILING DATE: 2004-11-09
 ; NUMBER OF SEQ ID NOS: 2112
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 214
 ; LENGTH: 2665
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-11-124-368A-214

 Query Match 3.5%; Score 98; DB 7; Length 2665;
 Best Local Similarity 20.8%; Pred. No. 15;
 Matches 80; Conservative 67; Mismatches 105; Indels 132; Gaps 19;

 QY 49 KEQKLGLENALIRLIDRGCEVIOIKSPSGRTTKQEPMLPALAICSGCSDISTK 108
 DB 1017 KKQDLKAKNTQTLTADVKNBIIIEOQRKIFSLIOEKNELOQ--MLESV-----IAEK 1066
 QY 109 QAAFAVSEVCRIPHLTFPIQFKKDLKESM-----KCGMGRALRK--AIADWYN 157
 DB 1067 E-----QKTDLKENIEMTIENOBELRLDDELKQOEIYAQEN 1106
 QY 158 ----EKGGWA-----LALAVTKYKQ-----RNG 176
 DB 1107 HAIKKEGELSRCDLAEVBEKLEKSOQLOEKQOOLLNVQEMSEMOKKINEIENLKN 1166
 QY 177 WSHKDLRLSHLKPSSSEGLAIVTKYTKMKWKEVHELKYKAL-----SVETEK--LKY 228
 DB 1167 LKNKE--LTLEHME--TERLELAQK--LNNYEEVKSIYTERKVKLKELOKSFETERDHLRGY 1222
 QY 229 LEAVKRV--KRTQDELEVIHL--IEBHR-----LVREHLITNHLKSKVW 269
 DB 1223 IREIATGLOTEBELKIAHILKEHOETIDELRVSSEKTAQIINTQDEKSHTKQBEI 1282
 QY 270 KALLQEMPLTALRLNGKMTANSVLEPGNSEVSLVCEKLCNEKLLKARIRHFFHILALE 329
 DB 1283 PVLHEEQ---ELLPRVKEV---SETQETNNELELLTEOSTTQDSTTLARIEM----- 1328
 QY 330 TYKTGHGLRGKLMRPDEBIILKAL 353
 DB 330 TYKTGHGLRGKLMRPDEBIILKAL 353

DB 1329 -----ERLRINEKFQESQOEIRKSL 1347

 RESULT 5
 US-11-124-368A-215
 ; Sequence 215, Application US/11124368A
 ; Publication No. US20050287559A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Michele Cargill
 ; APPLICANT: James J. Devlin
 ; APPLICANT: May Luke
 ; TITLE OF INVENTION: Genetic Polymorphisms Associated with
 ; TITLE OF INVENTION: Vascular Diseases, Methods of Detection and Uses Thereof
 ; FILE REFERENCE: CLO01524
 ; CURRENT APPLICATION NUMBER: US/11/124,368A
 ; CURRENT FILING DATE: 2005-05-09
 ; PRIOR APPLICATION NUMBER: US 60/568,845
 ; PRIOR FILING DATE: 2004-05-07
 ; PRIOR APPLICATION NUMBER: US 60/625,936
 ; PRIOR FILING DATE: 2004-11-09
 ; NUMBER OF SEQ ID NOS: 2112
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 215
 ; LENGTH: 2668
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-11-124-368A-215

 Query Match 3.5%; Score 98; DB 7; Length 2668;
 Best Local Similarity 20.8%; Pred. No. 15;
 Matches 80; Conservative 67; Mismatches 105; Indels 132; Gaps 19;

 QY 49 KEQKLGLENALIRLIDRGCEVIOIKSPSGRTTKQEPMLPALAICSGCSDISTK 108
 DB 1017 KKQDLKAKNTQTLTADVKNBIIIEOQRKIFSLIOEKNELOQ--MLESV-----IAEK 1066
 QY 109 QAAFAVSEVCRIPHLTFPIQFKKDLKESM-----KCGMGRALRK--AIADWYN 157
 DB 1067 E-----QKTDLKENIEMTIENOBELRLDDELKQOEIYAQEN 1106
 QY 158 ----EKGGWA-----LALAVTKYKQ-----RNG 176
 DB 1107 HAIKKEGELSRCDLAEVBEKLEKSOQLOEKQOOLLNVQEMSEMOKKINEIENLKN 1166
 QY 177 WSHKDLRLSHLKPSSSEGLAIVTKYTKMKWKEVHELKYKAL-----SVETEK--LKY 228
 DB 1167 LKNKE--LTLEHME--TERLELAQK--LNNYEEVKSIYTERKVKLKELOKSFETERDHLRGY 1222
 QY 229 LEAVKRV--KRTQDELEVIHL--IEBHR-----LVREHLITNHLKSKVW 269
 DB 1223 IREIATGLOTEBELKIAHILKEHOETIDELRVSSEKTAQIINTQDEKSHTKQBEI 1282
 QY 270 KALLQEMPLTALRLNGKMTANSVLEPGNSEVSLVCEKLCNEKLLKARIRHFFHILALE 329
 DB 1283 PVLHEEQ---ELLPRVKEV---SETQETNNELELLTEOSTTQDSTTLARIEM----- 1328
 QY 330 TYKTGHGLRGKLMRPDEBIILKAL 353
 DB 1329 -----ERLRINEKFQESQOEIRKSL 1347

 RESULT 6
 US-10-453-372-1204
 ; Sequence 1204, Application US/10453372
 ; Publication No. US2006000323A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Alisbrook, et al.
 ; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHODS
 ; FILE REFERENCE: 21402-589 A
 ; CURRENT APPLICATION NUMBER: US/10/453,372
 ; CURRENT FILING DATE: 2003-06-03
 ; PRIOR APPLICATION NUMBER: 09/789390
 ; PRIOR FILING DATE: 2001-02-23

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; PRIOR APPLICATION NUMBER: 60/185967
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 09/823187
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/195792
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: 09/839446
; PRIOR FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: 60/199476
; PRIOR FILING DATE: 2000-03-25
; PRIOR APPLICATION NUMBER: 09/863776
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/208263
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: 09/939398
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 60/227800
; PRIOR FILING DATE: 2000-08-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1609
; SOFTWARE: CnursSeqdist version 0.1
; SEQ ID NO 1204
; LENGTH: 600
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-453-372-1204
```

Query Match 3.4%; Score 95.5; DB 6; Length 600;

Best Local Similarity 18.8%; Pred. No. 2.9;

Matches 91; Conservative 78; Mismatches 191; Indels 123; Gaps 20;

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QY 95 ALAICSCSDISTQQAFAKAVSEV-----CRIFTHLFTFIOPK-----DL 135
DB 7 SVEICVSCSVSEVENVLYVNCSEKSVYRPNQKPEPMSFTHLNFQNNFNLITYPNTLNF 66
QY 136 KESNKCQMGGRALRKALADWYNEKGMALALAVTKYKQKRGWSHKDL-----LRLSHLKP 190
DB 67 SHAVALHGNKKQ-----NIEGAFILGSLTKQHLNNNELKILRADTFGLIENLEY 119
QY 191 SSEGLAVTKYITKGMEVHELYEKALSVTEKLLKYLEAVEKVKRTKDELEVIHLEE 250
DB 120 LQADYNLI-KYIERG--AFNKLHLKVL-IINDMLISPL-----P 155
QY 251 HRLVREHLTNHLKSKEVWKALLOEMPLTALLRLNGKMTANSVLE-PGNSEVSLVCEKLC 309
DB 156 DNIFRFASLT-HL---DIRGNRIQKLPYIGVLEHIGVLEQLQEDNPNWNSCDLLPLKAW 211
QY 310 NEKLKKARLHPHILALETKYTGHLRGKLRKRPDEELIKALDAAFYKTFKTEVPTGK 369
DB 212 LENM-----PYNIVYGEALCETPSDLYGRLL-----LKETNK 242
QY 370 RFLAADVVSAMORVLG-----SILNASTYAAAMCMVYTRTEKDSYVVAASDEVNP 421
DB 243 QELCPMGTSDFVRLIPPSQLENGYTPNGHTTQTSLHRLVYTRPKPTNSKISG-IVA 301
QY 422 CPVTTDMTLQOVLMAMSOIPAGGTDGSLPMIWAOKTNPADVFIYFTDNETFAGVHPAI 481
DB 302 GKALSNRLISOIVSYQTRVPP-LTPCPAPCC--KTH-PSDLGSLVNCQEKNIQSMSELI 357
QY 482 ALREYRKMDIPAKLIYCGMTSNGFTIADPDRGMLDMCGFDTGAL-----DVIR 531
DB 358 PKPLNAKKLHV-----NGNSIKDVDPVSDFTPEBGDLHLHLSNQITVIAKGVFHH 406
QY 532 NPT 534
DB 407 NLT 409
```

RESULT 7
US-10-453-372-1210
; Sequence 1210, Application US/10453372
; Publication No. US2006000323A1
; GENERAL INFORMATION:

```

; APPLICANT: Alisbroock, et al.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHODS
; FILE REFERENCE: 21402-589 A
; CURRENT APPLICATION NUMBER: US/10/453,372
; PRIOR FILING DATE: 2003-06-03
; PRIOR APPLICATION NUMBER: 09/789390
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/185967
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 09/823187
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/195792
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: 09/839446
; PRIOR FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: 60/199476
; PRIOR FILING DATE: 2000-03-25
; PRIOR APPLICATION NUMBER: 09/863776
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/208263
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: 09/939398
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 60/227800
; PRIOR FILING DATE: 2000-08-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1609
; SOFTWARE: CnursSeqdist version 0.1
; SEQ ID NO 1210
; LENGTH: 819
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-453-372-1210
```

Query Match 3.4%; Score 95.5; DB 6; Length 819;

Best Local Similarity 18.8%; Pred. No. 4.6;

Matches 91; Conservative 78; Mismatches 191; Indels 123; Gaps 20;

```

QY 95 ALAICSCSDISTQQAFAKAVSEV-----CRIFTHLFTFIOPK-----DL 135
DB 5 SVEICVSCSVSEVENVLYVNCSEKSVYRPNQKPEPMSFTHLNFQNNFNLITYPNTLNF 64
QY 136 KESNKCQMGGRALRKALADWYNEKGMALALAVTKYKQKRGWSHKDL-----LRLSHLKP 190
DB 65 SHAVALHGNKKQ-----NIEGAFILGSLTKQHLNNNELKILRADTFGLIENLEY 117
QY 191 SSEGLAVTKYITKGMEVHELYEKALSVTEKLLKYLEAVEKVKRTKDELEVIHLEE 250
DB 118 LQADYNLI-KYIERG--AFNKLHLKVL-IINDMLISPL-----P 153
QY 251 HRLVREHLTNHLKSKEVWKALLOEMPLTALLRLNGKMTANSVLE-PGNSEVSLVCEKLC 309
DB 154 DNIFRFASLT-HL---DIRGNRIQKLPYIGVLEHIGVLEQLQEDNPNWNSCDLLPLKAW 209
QY 310 NEKLKKARLHPHILALETKYTGHLRGKLRKRPDEELIKALDAAFYKTFKTEVPTGK 369
DB 210 LENM-----PYNIVYGEALCETPSDLYGRLL-----LKETNK 240
QY 370 RFLAADVVSAMORVLG-----SILNASTYAAAMCMVYTRTEKDSYVVAASDEVNP 421
DB 241 QELCPMGTSDFVRLIPPSQLENGYTPNGHTTQTSLHRLVYTRPKPTNSKISG-IVA 299
QY 422 CPVTTDMTLQOVLMAMSOIPAGGTDGSLPMIWAOKTNPADVFIYFTDNETFAGVHPAI 481
DB 300 GKALSNRLISOIVSYQTRVPP-LTPCPAPCC--KTH-PSDLGSLVNCQEKNIQSMSELI 355
QY 482 ALREYRKMDIPAKLIYCGMTSNGFTIADPDRGMLDMCGFDTGAL-----DVIR 531
DB 356 PKPLNAKKLHV-----NGNSIKDVDPVSDFTPEBGDLHLHLSNQITVIAKGVFHH 404
QY 532 NPT 534
DB 405 NLT 407
```

RESULT 8
US-11-147-047-32
Sequence 32, Application US/11147047
Publication No. US2005026068A1
GENERAL INFORMATION:
APPLICANT: Agarwal, Pankaj
APPLICANT: Murdoch, Paul R.
APPLICANT: Rizvi, Safia K.
APPLICANT: Smith, Randall P.
APPLICANT: Xiang, Zhaoying
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GP50016
CURRENT APPLICATION NUMBER: US/11/147,047
PRIORITY FILING DATE: 2005-06-07
PRIOR APPLICATION NUMBER: US/10/221,097
PRIOR FILING DATE: 2002-09-06
PRIOR APPLICATION NUMBER: PCT/US01/071143
PRIOR FILING DATE: 2001-03-05
PRIOR APPLICATION NUMBER: 60/187,107
PRIOR FILING DATE: 2000-03-06
PRIOR APPLICATION NUMBER: 60/236,874
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/188,916
PRIOR FILING DATE: 2000-03-13
PRIOR APPLICATION NUMBER: 60/237,846
PRIOR FILING DATE: 2000-10-03
NUMBER OF SEQ ID NOS: 52
SOFTWARE: ParseSeq for Windows Version 3.0
SEQ ID NO 32
LENGTH: 866
TYPE: PRT
ORGANISM: Homo sapiens
US-11-147-047-32

Query Match 3.4%; Score 95.5; DB 7; Length 866;
Best Local Similarity 18.8%; Pred. No. 4.9;
Matches 91; Conservative 78; Mismatches 191; Indels 123; Gaps 20;

95 ALAIGSGSDISTKQAAFAVSEV-----CRIPHLFTFIQFK-----DL 135
52 SVEICNVCSCVSEVENVLYNCEKVSVPYRNQKPEPMSNFYHLNFQNNFLNLYPNTFLNF 111
136 KESMKCGMWRALRKALADWYNEKGMALALAVTKYKORNGSHKDL-----LRLSHLKP 190
112 SHAVSLHLGNKDLQ-----NIEGAFIQLSALKQHLNNNELKILRADTFIGIENLEY 164
191 SSEGLAIVTKYITKGKVEVHELYKEKALSVETEKILKYLEAVKVKRTQDELEVHILIEE 250
165 LQADVNYLI-KYIERG--AFNKLHKLKVL--ILNDNLISFL-----P 200
251 HRLVREHLITNHLKSGEWMKALLQEMPLTALLNLGKMTANSVLE--PGNSEVSLVCEKLC 309
201 DNIFFRASLT-HL--DIRGNRIQKLPYIGVLEHIGVLELQLEDNPMWNCSDLLPLKAW 256
310 NEKLTKKARIHPHILIALETYKTHGRLGKLMKRPDEBILKALDAFYKTFKTVERTGK 369
257 LEMN-----PNIYIIGAICETPSDLYGRL-----LKEITNK 287
370 RFLLAADVASAMNQRYLG-----SINASTVAAMCMVTRTEKDSYVVAFSDMP 421
288 QELCPMGTSDFVRLILPESQLENGYTTPNGHTTQTSILHRLVTKPKPTNPSKISG-IVA 346
422 CPVTTMTLQOVVMAANSQIPAGTDCSLPMIWAOKTNTPADVPIVFTDNETFAGVHPAI 481
347 GKALSRNLSQIVSYQTRVPP-LTPCPAPCFG--KTH-PSDLGLSVNCEKAIQSNSELI 402
482 ALBRYRKMDIPAKLIVCGMTSNGFTIADPDDRGMLDMCGFDTGAL-----DVIR 531
403 PKRLNKKGLAHV-----NGNSIKQVDVSDFTDFBGLDILLHGSNQNIYIVIKQGVFH 451
532 NPT 534

Db 452 NPT 454

RESULT 9
US-10-453-372-1202
Sequence 1202, Application US/10453372
Publication No. US2006000323A1
GENERAL INFORMATION:
APPLICANT: Alsobrook, et al.
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHODS
FILE REFERENCE: 21402-589 A
CURRENT APPLICATION NUMBER: US/10/453,372
PRIOR FILING DATE: 2003-06-03
PRIOR APPLICATION NUMBER: 09/789390
PRIOR FILING DATE: 2001-02-23
PRIOR APPLICATION NUMBER: 60/185967
PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: 09/823187
PRIOR FILING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: 60/195792
PRIOR FILING DATE: 2000-03-10
PRIOR APPLICATION NUMBER: 09/839446
PRIOR FILING DATE: 2001-03-19
PRIOR APPLICATION NUMBER: 60/199476
PRIOR FILING DATE: 2000-03-25
PRIOR APPLICATION NUMBER: 09/863776
PRIOR FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: 60/208263
PRIOR FILING DATE: 2000-05-31
PRIOR APPLICATION NUMBER: 09/939398
PRIOR FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: 60/227800
PRIOR FILING DATE: 2000-08-25
Remaining Prior Application data removed - See file wrapper or PAM.
NUMBER OF SEQ ID NOS: 1609
SOFTWARE: CuraseqList version 0.1
SEQ ID NO 1202
LENGTH: 876
TYPE: PRT
ORGANISM: Homo sapiens
US-10-453-372-1202

Query Match 3.4%; Score 95.5; DB 6; Length 876;
Best Local Similarity 18.8%; Pred. No. 5;
Matches 91; Conservative 78; Mismatches 191; Indels 123; Gaps 20;

95 ALAIGSGSDISTKQAAFAVSEV-----CRIPHLFTFIQFK-----DL 135
62 SVEICNVCSCVSEVENVLYNCEKVSVPYRNQKPEPMSNFYHLNFQNNFLNLYPNTFLNF 121
136 KESMKCGMWRALRKALADWYNEKGMALALAVTKYKORNGSHKDL-----LRLSHLKP 190
122 SHAVSLHLGNKDLQ-----NIEGAFIQLSALKQHLNNNELKILRADTFIGIENLEY 174
191 SSEGLAIVTKYITKGKVEVHELYKEKALSVETEKILKYLEAVKVKRTQDELEVHILIEE 250
175 LQADVNYLI-KYIERG--AFNKLHKLKVL--ILNDNLISFL-----P 210
251 HRLVREHLITNHLKSGEWMKALLQEMPLTALLNLGKMTANSVLE--PGNSEVSLVCEKLC 309
211 DNIFFRASLT-HL--DIRGNRIQKLPYIGVLEHIGVLELQLEDNPMWNCSDLLPLKAW 266
310 NEKLTKKARIHPHILIALETYKTHGRLGKLMKRPDEBILKALDAFYKTFKTVERTGK 369
267 LEMN-----PNIYIIGAICETPSDLYGRL-----LKEITNK 297
370 RFLLAADVASAMNQRYLG-----SINASTVAAMCMVTRTEKDSYVVAFSDMP 421
298 QELCPMGTSDFVRLILPESQLENGYTTPNGHTTQTSILHRLVTKPKPTNPSKISG-IVA 356
422 CPVTTMTLQOVVMAANSQIPAGTDCSLPMIWAOKTNTPADVPIVFTDNETFAGVHPAI 481

Db 357 GKALSNRNLQIIVSYQTRVPP-LTPCPAPFC--KTH-PSDLGLSVNCOEKNIQMSBELI 412
QY 482 ALREYRKMDIPAKLIYCGMTSNGFTIADPPDRGMLDMCGEPTGAL-----DYIR 531
Db 413 PKPLNAKRLHV-----NGNSIKDVDSDFTFEGDLHLHLSNQITVIKGVFH 461
QY 532 NPT 534
Db 462 NLT 464

RESULT 10
US-10-453-372-1208
; Sequence 1208, Application US/10453372
; Publication No. US2006003323A1
; GENERAL INFORMATION:
; APPLICANT: Alcobrook, et al.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-589 A
; CURRENT APPLICATION NUMBER: US/10/453,372
; PRIOR FILING DATE: 2003-06-03
; PRIOR APPLICATION NUMBER: 09/789390
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/185967
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 09/823187
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/195792
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: 09/839446
; PRIOR FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: 60/199476
; PRIOR FILING DATE: 2000-03-25
; PRIOR APPLICATION NUMBER: 09/863776
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/208263
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: 09/939398
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 60/227800
; PRIOR FILING DATE: 2000-08-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1609
; SOFTWARE: Cureseqdist version 0.1
; SEQ ID NO 1208
; LENGTH: 876
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-453-372-1208

Query Match 3.4%; Score 95.5; DB 6; Length 876;
Best Local Similarity 18.8%; Pred. No. 5;
Matches 91; Conservative 78; Mismatches 191; Indels 123; Gaps 20;

QY 95 ALAICSCSDISTKQAFKAVSEV-----CRIFTHLFTFIQFK-----DL 135
Db 62 SVEICNVSCSVSEVNVLYNCEKSVYRPNQKRPWSFPHILNQNNLNLITPTFLNF 121
QY 136 KESMKCGMGARLAKALADWYNEKGMLALAVTYKQKONGMSKDL-----LRLSHKP 190
Db 122 SHAVSLHGNKQLQ-----NIEGAPFLGSLAKQLHNNNELKITLADTFLGIEMLY 174
QY 191 SSEGLATVTKYTKGWKVEVHELYEKALSVETBKLLKLEAVEKVKRKDELEVHLIE 250
Db 175 LQADVNLI-KYIERG--AFNKLHLKVL--ILNDNLISFL-----P 210
QY 251 HRLVREHLTYNHLKSKEVWKKALLOEMPLTALLRNLGKMTANSVLE--PGNSEVSYCEKLC 309
Db 211 DNIRFPASLT-HL--DIRGNRIQKLPYIGVLEHIGRVEVQLDENPNWNCSDLLPLKAW 266
QY 310 NEKLKKARHPHILALETVTKGHGRGKLKMRPDEEILKALDAFYKTFKVEPTGK 369
Db 267 LENN-----PYNIVIGBAICETPSDLYGRL-----LKETNK 297

QY 370 RFLIADVSAQMQRVLG-----SILNASTVAAAMCVVTRTEKDSYVAFSDENVP 421
Db 298 QELCEPMGTSGDFVRIILPESQLENGYTPPTNGHTTQISLHLYLPPRTTPSKISG-IVA 356
QY 422 CPVTTDMTLQOVLVAMASQIPAGTDCSLPMIWAQKTPADVFIPTDNETPAGVHPAI 481
Db 357 GKALSNRNLQIIVSYQTRVPP-LTPCPAPFC--KTH-PSDLGLSVNCOEKNIQMSBELI 412
QY 482 ALREYRKMDIPAKLIYCGMTSNGFTIADPPDRGMLDMCGEPTGAL-----DYIR 531
Db 413 PKPLNAKRLHV-----NGNSIKDVDSDFTFEGDLHLHLSNQITVIKGVFH 461
QY 532 NPT 534
Db 462 NLT 464

RESULT 11
US-10-878-556A-113
; Sequence 113, Application US/10878556A
; Publication No. US20050266399A1
; GENERAL INFORMATION:
; APPLICANT: Hoffmann La-Roche Inc.
; TITLE OF INVENTION: HCV regulated protein expression
; FILE REFERENCE: 21762
; CURRENT APPLICATION NUMBER: US/10/878,556A
; PRIOR FILING DATE: 2004-06-28
; NUMBER OF SEQ ID NOS: 199
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 113
; LENGTH: 858
; TYPE: PRT
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: sw_hum/ubp5_human
; DATABASE ENTRY DATE: 1996-02-01
US-10-878-556A-113

Query Match 3.4%; Score 95; DB 6; Length 858;
Best Local Similarity 20.0%; Pred. No. 5.3;
Matches 120; Conservative 85; Mismatches 217; Indels 178; Gaps 34;

QY 37 LCPFSGEGTYIKQKGLSEVNAALI-----RLIBDGRGCEVIOEIKSFQEGRTTKQ 90
Db 99 LAIGVEGG-EDLSSEKTELEDVQIVLPDYLEIARQGLG-----GLPDIYRDVTSAYE 152
QY 91 PMLPALAICSCSDISTKQAFKAVSEVCRIPTHLFTFIQFKDLK-----ESMKCGMW 144
Db 153 ALISA-----DSASRKQEVQAWDGEVRQVSKAFSLKQLDNPARIIPCGMKCSKCDM- 204
QY 145 GRALRKALADWYNEKGMLALAVTYKQKONGMSHKKDLRLSHKPSSEGLATVTKYTK 204
Db 205 ---RENL--WLNLTDS--ILCGRRYFDSSGGNNH--AAEHYRETYPLAVKLGTTTP 253
QY 205 GWKEVHELYEKALSVETBKLLKYLE-----AVEKVKRKDELEVHLIEBRLVREH 257
Db 254 DGADVYS-YDEDDMYLD-PSLAELHSHFGIDMLKMQGTDKTMTELE-----IDMNGRIGE- 306
QY 258 LITNHLKSKEVWKKALQE--MPLTAL-----LRNIGKMT-ANSVLEPGNSEVSL--V 304
Db 307 -----WE-LIQSGVPLKPLFGPGYTGIRNGNSCYLNSVQVLPSPDPQRKY 354
QY 305 CEKLCNEKLKKARHP---PHILALETYTKGHGLGKLKMRPDEE----- 348
Db 355 VDKL--EKIPQNAETPDTPDSTQVA---KLGGHLSGEYSKVPSPSGDGERVPEQEV 408
QY 349 -----ILKALDAAPFKTFKT-VEPTGKRPFLAV-----DVASMMQVRVLSILNAST 394
Db 409 QDGIAPMKFRLIKGHPERSTNRQDAQEFLLHIMVVENCSSEBNPVPFLVBEK 468
QY 395 VAAAMCVVTRTEKDSYVAFSDENVPCPVTTDMTLQOVL-----MA 436
Db 436

Db 469 IKCLATEKVKYTORVDYIM-----QLPVMDALNKEELLEVEEKKQAEKKALPELV 523
 QY 437 MSQIP-----AGTDCSLPMIW-----AQKTPA---DVFIPTNPPAGVH 478
 Db 524 RAQVPSSCLEAYGAPEQVDFWSTALQAKSVAAVKTTFASFPPDVLVIQIKKFTF----- 578
 QY 479 PALILREKKMDI-----PALIYCGMTSNGF-----TIADPD-RCGLDWCW 521
 Db 579 ---GLDWVPKLDVSIEMPEELDISQLKGTGLQEGEELPDIAPLVTPDEPKGSLGYG 635

RESULT 12

US-10-467-657-3988
 ; Sequence 3988, Application US/10467657
 ; Publication No. US20050260581A1
 ; GENERAL INFORMATION:
 ; APPLICANT: CHIRON SPA
 ; APPLICANT: FONTANA Maria Rita
 ; APPLICANT: PIZZA Mariagrazia
 ; APPLICANT: MASIGNANI Vega
 ; APPLICANT: MONACI Elisabetta
 ; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
 ; FILE REFERENCE:
 ; CURRENT APPLICATION NUMBER: US/10/467,657
 ; CURRENT FILING DATE: 2003-08-11
 ; PRIOR APPLICATION NUMBER: GB-0103424.8
 ; PRIOR FILING DATE: 2001-02-12
 ; NUMBER OF SEQ ID NOS: 9218
 ; SOFTWARE: SeqMan99, version 1.04
 ; SEQ ID NO 3988
 ; LENGTH: 612
 ; TYPE: PRT
 ; ORGANISM: Neisseria gonorrhoeae
 US-10-467-657-3988

Query Match 3.4%; Score 94; DB 6; Length 612;

Best Local Similarity 21.5%; Pred. No. 4; Matches 69; Conservative 54; Mismatches 138; Indels 60; Gaps 11;

QY 40 GSEGGTYIYKEQKLGLENALIRLIEDRGCEVIOEIKFSQEGRTTKQEPMLPALAIC 99
 Db 148 GAKGCGNPRKGAKEKDYTSANKKASDNGKAVQDKKTEBKNAKTDSDLKAAVAA 207
 QY 100 SQCSDISTKQAAFKAVSEVCRIPTLFTFIQPKDKESMKCGMGRALKAIADWNEK 159
 Db 208 T--NVEVENKALLKQSEGMLHVSLSLKQLOEERIRQERIR--QERIRQA-----R 254
 QY 160 GGMALALAVTKYKONGS-----HKDLRL-----SHLKSSSEGL 195
 Db 255 GN-----LASVNRKQHEAMDKFQKLNTLNRLLKTEVAATQAISRFGSGNYKNSRPAAVAL 310
 QY 196 AI-----VTKYITGKMK--VHELYK-EKALSVEETEKLLKYLEAVEKVKRTKD 240
 Db 311 FAKNAEPGQKRFRLKTRYVANSNREVVQDLEKQKALAVQEKINELARKLQIQAQV 370
 QY 241 ELEVLHLEEHRLVREHLITNHLKSKKXVKALLQ---EMPTALLNLNIGKMTANSVLEFG 297
 Db 371 SLKKQGVTDAAEQTESRRQNAKISDKARKLEQKNGEOQLNLSLNEKKAEHRIDDA 430
 QY 298 NSESVLVECKL-CNEKLLKKA 317
 Db 431 EAKRKLAENKLAAREKARKEA 451

RESULT 13

US-11-052-554A-130
 ; Sequence 130, Application US/11052554A
 ; Publication No. US2005028866A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Sachdeva, et al.
 ; TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE
 ; PROTEINS OF THERAPEUTIC POTENTIAL
 ; FILE REFERENCE: 30853/40359A

; CURRENT APPLICATION NUMBER: US/11/052,554A
 ; CURRENT FILING DATE: 2005-02-07
 ; PRIOR APPLICATION NUMBER: US 60/589,227
 ; PRIOR FILING DATE: 2004-07-20
 ; PRIOR APPLICATION NUMBER: IN 173/DEL/2004
 ; PRIOR FILING DATE: 2004-02-06
 ; NUMBER OF SEQ ID NOS: 763
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 130
 ; LENGTH: 1244
 ; TYPE: PRT
 ; ORGANISM: Mycoplasma pneumoniae
 US-11-052-554A-130

Query Match 3.4%; Score 94; DB 7; Length 1244;

Best Local Similarity 18.2%; Pred. No. 11; Matches 129; Conservative 96; Mismatches 209; Indels 276; Gaps 35;

QY 6 NOMOPLNEKOIANSODGVWQVTDMMNRHLRFLCFSEGGTYIYKEQKLGLENAE---AL 61
 Db 513 NSYSPIKRIRVNRSGTVV-----FGLDGGSYLLKQDSTNKKSVSKOSLYTL 558
 QY 62 IRLIEDRGCEVIOEIKFSQEGRTTKQEPMLPALAICQCSDISTKQAAKAVSEVCRI 121
 Db 559 LTKSSGSGNKKVLRDL-----DKOKQFL-----KERARQA-----KT 590
 QY 122 PTHLFTFIQPKDKESMKCGM-----GRALKAIADWNEKGMALALAVTKYK 172
 Db 591 NTFYSTNPAFSPFPINETIK--SWEDKRELLIANLVNASLD-QOKKASKALTEAFNRYK 647
 QY 173 -----QRNGSHKDLRLSHLK-----PSSEGLAVTKYI 202
 Db 648 ELIKFAPVALATTMISFYPPQMKALNNKLEBRANNLNQNNQANPTWINGLSAKLPYV 707
 QY 203 -TKG-----WKEVHELKKEKALSVEETEKLLKYLEAVEKVKR----- 237
 Db 708 NTNGVYEKLNNYFTPLITKTLMPKVQ--BETSISEBSNKKTKTADVDKIRDKILENIQ 765
 QY 238 --TDEBLE-----VHILIEHR-----LV 254
 Db 766 TKVNDPVRNKKLPALAPPAVSNTLLNVNNDKVLSSGANSLSLSDKVNPLSPMLL 825
 QY 255 REHLITNHL--KSKVWFKAL-----LOEMPLYT--ALIRNLG-----KMTA 290
 Db 826 KQAFPNNDLPFKAQQLFQDIOEKSSNNGMQSSSTTNDADALSKVIGNVYTTWAKLTD 885
 QY 291 NSVLEPGNSE-----VSLVECKLNEKLLK--KARIHPEHILIALETYKTVGGLRGK 340
 Db 886 KSIY--GNPKONKFPDLFLANFEASIDEKSFVVDKAVIDHYRFITYLQ----- 932
 QY 341 LKMRPDEILKALDAFYKTFTEVEPTGRF--LLAVDSASNM--QRVLGSIINA 392
 Db 933 --WLVDQKL-----KNFKSLKLTMLKFEVAFIYKNTETNFSNPQVGSFYFY 981
 QY 393 STVAANMCVVVTRTEKDSVVAFAFSDMBVCPVYTTMTLQOVLAMASQIPAGTDCSLPMI 452
 Db 982 ENSASAEVKESTQTLDPNFFY-----KTTIKPTVO--ALQOV-----ASIALV 1022
 QY 453 WAQKTNTPADVFIIVFTDNETPAGVHPA-----IALREYKKMDIPAKLIYVG 500
 Db 1023 QKQCMQONSTHGYFTGLSTSSMFDASSRAIILQITKTSLOQVSGSDQ--KLIIG 1080
 QY 501 WTSNGFTIADPDRGMLDMCGFDYGA-----LDVIRNFTLD 536
 Db 1081 -TNNQLLL-----DRIAVQLSGINPSTYNGSGKTIATYFQVDVAGNPTLD 1125

RESULT 14

US-10-878-556A-169
 ; Sequence 169, Application US/10878556A
 ; Publication No. US20050266399A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hoffmann La-Roche Inc.

```

1  TITLE OF INVENTION: HCV regulated protein expression
2
3  FILE REFERENCE: 21762
4
5  CURRENT APPLICATION NUMBER: US/10/878,556A
6
7  CURRENT FILING DATE: 2004-06-28
8
9  NUMBER OF SEQ ID NOS: 199
10
11 SOFTWARE: PatentIn version 3.1
12
13 SEQ ID NO 169
14
15 LENGTH: 1404
16
17 TYPE: PR1
18
19 ORGANISM: Homo sapiens
20
21 PUBLICATION INFORMATION:
22
23 DATABASE ACCESSION NUMBER: humangp/chr12-q14221
24
25 DATABASE ENTRY DATE: 2003-04-22
26
27 US-10-878-556A-169

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Query Match	3.4%;	Score 94;	DB 6;	Length 1404;
Best Local Similarity	23.9%;	Pred. No. 13;		
Matches 61;	Conservative 37;	Mismatches 83;	Indels 74;	Gaps 10;

OY	50	EOKL	GL	EN	BA	LR	IEDR	GC	EV	IO	ET	RS	--	FS	OE	GR	TR	KOE	PM	PA	AI	CS	CS	DIST	107
b	1046	EBK	LS	AO	ED	LS	NR	NO	IG	NO	NK	TI	OE	LT	AK	AL	EO	DA	CS	KE	EO	OL	---	---	1091

Qy	108	KQAFKAVSEVCRIP	THLETFIQKQDLKES	MGCMGWRALRKAI	ADWYNEKGGMALALA	167
				:	:	
b	1092	-QERCKALD-	-IQEKSLKEX-		-ELVNEKSKLA-	E 11211
		:	:	:	:	

Qy	168	VTKYKQNRGNSHDKDLRLSHLKPSSGGLAVTKYITKGMKEVHELYKEKOLSVETE----	223
Oy	1122	IEBTKCR---QEKBITKNEBELSKHLEST-----KEITYNKDAQOLLIDOOKLELO	1169

Qy 224 -KLKYLEAVEKQRTKDEVLVTHLIEBHVLRVHL-----LTNHLKSEVWKAALLQ-- 275

b 1170 GKDSLKKAIVEOEKRNQOLIKDQVKEEBELKKEFIEKALNHEIIEKEVEVMKKHENE 1229

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Qy      276 ----MPLTALLRNLG 286
          | : ||| |||
Db      1230 AKLTMOITALNENLG 1244

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RESULT 15
US-11-017-550-65

; sequence 65, Application US/11017550
 ; Publication No. US20050250183A1
 ; GENERAL INFORMATION:
 ; APPLICANT: The Scripps Research Inst

```

; APPLICANT: Schultz, Peter G
; APPLICANT: Wang, Lei
; APPLICANT: Anderson, John C
; APPLICANT: Chin, Jason

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; APPLICANT: Liu, David R
; APPLICANT: Magliery, Thomas
; APPLICANT: Meggers, Eric L
; APPLICANT: Mohl, Bryan A

```

; APPLICANT: Pasternak, Miro
; APPLICANT: Santoro, Stephen W
; APPLICANT: Zhang, Zhiwen

```
; FILE REFERENCE: 54-000120US  
;  
; CURRENT APPLICATION NUMBER: US/11/017,550  
;  
; CURRENT FILING DATE: 2004-12-17  
; DATE OF INFORMATION RECEIVED: 06/18/05 007
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PRIOR FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: US 60/285, 030
PRIOR FILING DATE: 2001-04-19

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; PRIOR FILING DATE: 2002-02-06
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn version 3.1

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; LENGTH: 932
; TYPE: PRT
; ORGANISM: Archaeoglobus fulgidus

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US-11-017-550-65

Query Match	3.4%	Score 93.5;	DB 7;	Length 932;
Best Local Similarly	23.0%;	Pred. NO. 8;		
Matches 46;	Conservative 42;	Mismatches 83;	Indels 29;	Gaps 8;

Qy 108 KQAAFKAVSEVCHPTHLFTFETPFK-KDLKESKMGCGMGRALRAIAD-----WYNKKG 160

Db 689 KENYLKEGVELTLDRLWVSRMGRRAIKEVREADNLTQTRRAVNAAFPEILNDVRYLRG 748

Qy 161 GMAIALAVTKY-KORNGNSHKDLIRLSHIKPSSEGLAIVTKYTTKGWKEVHELHYEKALIS 219
Db 749 GENIAIILDDWIKILAPAPHICIELMILKHS-----YYS--LESYPEDETTRD 797

Qy 220 VETEKTLKYL---EAEVKVKTKEDELEVIHL--IEBHRLVRBHLJTNHLSKSKEWKALL 273

Dh 798 RRRARRIEREFAPNTVEDIOIRIKKFSDADEVYIIPADPMWKAARAKVAESGDVGAMKKOLM 857

QY 274 QEMPTALLRNIGKMTANSV 293
| | | | |
ASR QNER---LRKIGKEVSNV 873

Search completed: January 13, 2006, 11:22:28
Job time : 33 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 13, 2006, 11:05:43 ; Search time 76 Seconds
(without alignments)
4994.398 Million cell updates/sec

Title: US-10-615-515-6
Perfect score: 2787
Sequence: 1 MBSSVNMQPLNKRQJANSQ.....MCGFDGALDVIRNFILDMI 538

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot_05.80:*
1: uniprot_sprotc:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2784	99.9	538	1 R060_HUMAN	P10155 homo sapien
2	2735	98.1	534	2 OS1J99_HUMAN	Q51J99 homo sapien
3	2732	98.0	534	2 Q86W13_HUMAN	Q86W13 homo sapien
4	2659	95.4	525	2 OS1J98_HUMAN	Q51J98 homo sapien
5	2657	95.3	518	2 OS1J98_HUMAN	Q51J98 homo sapien
6	2654	95.2	518	2 Q86W14_HUMAN	Q86W14 homo sapien
7	2541	91.2	538	1 R060_MOUSE	Q08562 mus musculu
8	2535	91.0	538	1 Q8R562_MOUSE	Q8R562 mus musculu
9	2532	90.9	538	2 Q8W12_MOUSE	Q8W12 mus musculu
10	2532	90.9	547	2 Q7T740_MOUSE	Q7T740 mus musculu
11	2269	81.4	538	1 R060_XENLA	P43700 xenopus lae
12	1544.5	55.4	547	2 Q4SP4A_TETNG	Q4SP4A tetradon n
13	1517	54.4	558	2 Q5M7X5_BRARE	Q5M7X5 brachydano
14	1265	45.4	244	2 OS1J97_HUMAN	Q51J97 homo sapien
15	1017.5	36.5	644	2 Q61K10_CABBR	Q61K10 caenorhabdi
16	1011	36.3	643	1 R060_CABEL	Q27274 caenorhabdi
17	861	30.9	552	2 Q852T5_9C4UD	Q852T5 mycobacteri
18	798.5	28.7	531	1 R060_DEIRA	Q9TAW6 deinosoccus
19	269.5	9.7	552	1 Q7UEC3_RHOBA	Q7UEC3 rhodospirill
20	255	9.1	514	2 Q4KEC3_PSEPF	Q4KEC3 pseudomonas
21	223	8.0	517	2 Q8ZLH8_SALTY	Q8ZLH8 salmonella
22	205	7.4	517	2 Q57IV5_SALCH	Q57IV5 salmonella
23	201	7.2	560	2 OS1MW2_STIRO	OS1MW2 silicibacte
24	189.5	6.8	637	2 Q9W4R7_DROME	Q9W4R7 drosophila
25	180.5	6.5	719	1 T880_TETTH	Q94818 tetrahymena
26	165.5	5.9	1187	2 Q6XKX0_MOUSE	Q6XKX0 mus musculu
27	143.5	5.1	712	2 Q6ZU09_HUMAN	Q6ZU09 homo sapien
28	133.5	4.8	1937	2 Q6SNT2_SHPERO	Q6SNT2 shimpereca c
29	132.5	4.8	786	2 Q91520_THYTH	Q91520 thunnus thy
30	132	4.7	654	2 Q6GUR8_GASAC	Q6GUR8 gasterosteus
31	132	4.7	1929	2 Q98T06_9PERC	Q98T06 notochenia

32	130.5	4.7	1936	2 Q90YF6_PARPO	Q90YF6 paracitrich
33	130.5	4.7	1937	1 MYH8_HUMAN	P13535 homo sapien
34	129.5	4.6	1938	1 MYSS_CHICK	P13538 gallus galli
35	129	4.6	975	2 Q98T05_9PERC	Q98T05 notochenia
36	128	4.6	799	2 Q4SSZ8_TETNG	Q4SSZ8 tetradon n
37	128	4.6	1938	2 Q8M4V0_HORSE	Q8M4V0 equus caball
38	127.5	4.6	1171	2 Q6DJR2_XENTR	Q6DJR2 xenopus tro
39	126	4.5	1938	2 Q91BD7_SERDU	Q91BD7 seriola dum
40	124.5	4.5	244	2 Q7PYC6_ANOGA	Q7PYC6 anopheles g
41	124.5	4.5	1935	2 MYSS_CYPCA	Q20339 cyprinus ca
42	124	4.4	766	2 Q51EZ2_ENTHI	Q51EZ2 entamoeba h
43	124	4.4	1937	1 MYH8_MOUSE	P13542 mus musculu
44	123	4.4	1939	2 Q9TV61_PIG	Q9TV61 sus scrofa
45	123	4.4	3616	2 Q9W6V0_CHICK	Q9W6V0 gallus galli

ALIGNMENTS

RESULT 1
R060_HUMAN STANDARD; PRT; 538 AA.
ID P10155; Q92787; Q9H1W6;
AC P10155; Q92787; Q9H1W6;
DT 01-MAR-1989 (Rel. 10, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE 60-kDa SS-A/Ro ribonucleoprotein (60 kDa Ro protein) (60 kDa
DE ribonucleoprotein Ro) (RoRNP) (Ro 60 kDa autoantigen) (TROVE domain
DE family member 2) (Sjogren syndrome type A antigen) (SS-A) (Sjogren
DE syndrome antigen A2).
GN Name=TROVE2; Synonyms=R060, SSA2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae;
OC Homo.
CX NCBI_TaxID=9606;
[1]
RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM LONG).
RX MEDLINE=89071722; PubMed=320833;
RA Deutscher S.L., Harley J.B., Keene J.D.,
RT "Molecular analysis of the 60-kDa human Ro ribonucleoprotein.",
RL Proc. Natl. Acad. Sci. U.S.A. 85:9479-9483(1988).
[2]
RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM LONG).
RX MEDLINE=89198084; PubMed=2649513;
RA Ben-Chetrit B., Gandy B.J., Tan B.M., Sullivan K.F.,
RT "Isolation and characterization of a cDNA clone encoding the 60-kD
RT component of the human SS-A/Ro ribonucleoprotein autoantigen.",
RL J. Clin. Invest. 83:1284-1292(1989).
[3]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA] (ISOFORM SHORT).
RA Buyon J.P., Didonato F., Tseng C.E., Raebbaum W., Morris A.,
RA Hamel J.C., Chan B.K.L.,
RT "Identification and characterization of an alternative mRNA transcript
RT of the 60-kD SS-A/Ro ribonucleoprotein encoding the N-terminal RNA
RT binding domain alone.",
RL Submitted (Oct-1996) to the EMBL/GenBank/DBJ databases.
[4]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RG Human chromosome 1 international sequencing consortium;
RL Submitted (Jul-2000) to the EMBL/GenBank/DBJ databases.
[5]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM LONG).
RC TISSUE=Testis;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Struhsberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shemen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.T., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Bronstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,

RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gumaratne P.H.,
 RA Richards S., Mowley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Nadeau A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smallus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RP INTERACTION WITH RIP1.
 RC TISSUE=Keratinocyte;
 RX MEDLINE=20015020; PubMed=10545525;
 RA Wang D., Buyon J.P., Zhu W., Chan E.K.L.,
 RT "Defining a novel 75-kDa phosphoprotein associated with SS-A/Ro and
 RT identification of distinct human autoantibodies.";
 RL J. Clin. Invest. 104:1265-1275(1999).
 CC FUNCTION: RNA-binding protein that binds to several small
 CC cytoplasmic RNA molecules known as Y RNAs. May stabilize these
 CC RNAs from degradation.
 CC -Y- SUBUNIT: Binds RIP1.
 CC -I- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -I- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=Long;
 CC IsoId=PI0155-1; Sequence=Displayed;
 CC Name=Short; Synonyms=60E2;
 CC IsoId=PI0155-2; Sequence=VSP_005911, VSP_005912;
 CC -I- DISEASE: Sera from patients with systemic lupus erythematosus
 CC (SLE) often contain antibodies that react with the normal cellular
 CC SS-A2 protein as if this antigen was foreign.
 CC -I- SIMILARITY: Belongs to the Ro 60 kDa family.
 CC -I- SIMILARITY: Contains 1 TROVE domain.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC EMBL: J04137; AAA35493.1; -; mRNA.
 CC EMBL: M25077; AAA35532.1; -; mRNA.
 CC EMBL: U44388; AAB81552.1; ALT_TERM; Genomic_DNA.
 CC EMBL: U44388; AAB81553.1; -; Genomic_DNA.
 CC EMBL: AL136370; CAC17589.1; -; Genomic_DNA.
 CC EMBL: BC036658; AA336658.1; -; mRNA.
 CC PIR: A31760; A31760.
 CC EMBL: ENSG00000116747; Homo sapiens.
 CC DR HGNC: HGNC:11313; TROVE2.
 CC DR MIM: 600063; -.
 CC DR MIM: 234700; -.
 CC DR GO: GO:0030529; C:ribonucleoprotein complex; TAS.
 CC DR GO: GO:0003723; F:RNA binding; TAS.
 CC DR GO: GO:0006383; P:transcription from RNA polymerase III promoter; TAS.
 CC DR InterPro: IPR008858; TROVE.
 CC DR Pfam: PF05731; TROVE; 1.
 CC DR PROSITE: PS50988; TROVE; 1.
 CC DR Alternative splicing; Antigen; Ribonucleoprotein; RNA-binding;
 CC KM Systemic lupus erythematosus.
 CC PT DOMAIN 16 369 TROVE.
 CC VARSPLIC 195 205 LAITYKITYTG -> KKKIFIKKKG (in isoform
 CC Short).
 CC FT VARSPLIC 206 538 /Frid=VSP_005911.
 CC FT CONFLICT 239 239 /Frid=VSP_005912.
 CC FT CONFLICT 515 538 R -> K (in Ref. 1).
 CC FT GMLDMGPDVTGALDVINFTLDMT -> ALQNTILINKSF
 CC (in Ref. 2).
 CC SQ SEQUENCE 538 AA; 60671 MW; CD735B1DF2B13098 CRC64;

Query Match 99.9%; Score 2784; DB 1; Length 538;
 Best Local Similarity 99.8%; Pred. No. 3,4e-178;
 Matches 537; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MEESVNOVOPLNKQIANSQDGVVQVDTMNRHLRFLCRSGEGTYIKKQKIGLENAEA 60
 DB 1 MEESVNOVOPLNKQIANSQDGVVQVDTMNRHLRFLCRSGEGTYIKKQKIGLENAEA 60
 QY 61 LRLIDGGGCEYIOGKISFSGSGRTTKOEPMLFALISQSGDSTKQAFRAVSEVCR 120
 DB 61 LRLIDGGGCEYIOGKISFSGSGRTTKOEPMLFALISQSGDSTKQAFRAVSEVCR 120
 QY 121 IPTHLFTPIQFKDLKESMKCGMGRALKALADWYNEKGMALALAVTKYKQKNGSHK 180
 DB 121 IPTHLFTPIQFKDLKESMKCGMGRALKALADWYNEKGMALALAVTKYKQKNGSHK 180
 QY 181 DLRLSHLKPSSSGALIVTKYITGKMEVHELYEKALSVETKLLKYLAVERKVKTKD 240
 DB 181 DLRLSHLKPSSSGALIVTKYITGKMEVHELYEKALSVETKLLKYLAVERKVKTKD 240
 QY 241 ELEVTILIEBHLYREHLLTNHLKSKKWKALLQEMPLTALLBNLGKMTANSVLBPNSG 300
 DB 241 ELEVTILIEBHLYREHLLTNHLKSKKWKALLQEMPLTALLBNLGKMTANSVLBPNSG 300
 QY 301 VSLVCEKLCNEKLLKKARLHPHILLALETYKTHGLRGKLKMRPDEILKALDAAFYKT 360
 DB 301 VSLVCEKLCNEKLLKKARLHPHILLALETYKTHGLRGKLKMRPDEILKALDAAFYKT 360
 QY 361 EKTVEPTGRFLIADVSAANQVIGSILINASTVAANCMVTRTRBKDSYVAFSDENV 420
 DB 361 EKTVEPTGRFLIADVSAANQVIGSILINASTVAANCMVTRTRBKDSYVAFSDENV 420
 QY 421 PCVPTTDMTLQVULMMSQIPAGCTDCSLPMIAQKTNTPADVFYFTDNETFAGGVHRA 480
 DB 421 PCVPTTDMTLQVULMMSQIPAGCTDCSLPMIAQKTNTPADVFYFTDNETFAGGVHRA 480
 QY 481 IALREYRKMDIPAKLIVCGMTSNGFTIADPDDRGMLDMGPFDTGALDVIRNFTLDMT 538
 DB 481 IALREYRKMDIPAKLIVCGMTSNGFTIADPDDRGMLDMGPFDTGALDVIRNFTLDMT 538
 RESULT 2
 ID 05LJ99 HUMAN PRELIMINARY; PRT; 534 AA.
 AC 05LJ99_
 DT 01-FEB-2005 (T:EMBLrel. 29, Created)
 DT 01-FEB-2005 (T:EMBLrel. 29, Last sequence update)
 DT 01-FEB-2005 (T:EMBLrel. 29, Last annotation update)
 DE Sjogren syndrome antigen A2 (60kDa, ribonucleoprotein autoantigen SS-A/Ro).
 GN Name=SSA2; ORFName=RP11-101E13.3-005;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 CX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Whitehead S.;
 RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
 RL EMBL: AL136370; CA110823.1; -; Genomic DNA.
 DR GO: GO:0030529; C:ribonucleoprotein complex; IEA.
 DR GO: GO:0004618; F:phosphoglycerate kinase activity; IEA.
 DR GO: GO:0003723; F:RNA binding; IEA.
 DR GO: GO:0006096; P:glycolysis; IEA.
 DR InterPro: IPR001576; PGK.
 DR InterPro: IPR008858; TROVE.
 DR Pfam: PF05731; TROVE; 1.
 DR PROSITE: PS50988; TROVE; 1.
 DR Ribonucleoprotein; Vital nucleoprotein.
 KM Ribonucleoprotein; Vital nucleoprotein.
 SQ SEQUENCE 534 AA; 60169 MW; 785F949FED553344 CRC64;
 Query Match 98.1%; Score 2735; DB 2; Length 534;

Best Local Similarity 99.8%; Pred. No. 6,4e-175;
Matches 527; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MESSVNQOPLNEKQIANSODGYVQVTDNMRLHRLFLCGSEGGTYIYKEQKLGLENBA 60
DB 1 MESSVNQOPLNEKQIANSODGYVQVTDNMRLHRLFLCGSEGGTYIYKEQKLGLENBA 60

QY 61 LIRLIEDRGCEVIOEIKSFQSEGRITTKOEPMLFALAI CSQCSDISTKQAFKAVSEVCR 120
DB 61 LIRLIEDRGCEVIOEIKSFQSEGRITTKOEPMLFALAI CSQCSDISTKQAFKAVSEVCR 120

QY 121 IPTHLFTFIQPKODKESMKCGMWRALRAIADWYNEKGMALALAVTKYKQRNGWSHK 180
DB 121 IPTHLFTFIQPKODKESMKCGMWRALRAIADWYNEKGMALALAVTKYKQRNGWSHK 180

QY 181 DLRLSHLKSSSEGLAVTKYITKGMEVHELYEKKALSVETELKYLEAVEKVKTRD 240
DB 181 DLRLSHLKSSSEGLAVTKYITKGMEVHELYEKKALSVETELKYLEAVEKVKTRD 240

QY 241 ELBYIHILIEBRLVREHLTNHLKSKEVWKLLOEMPLTALLRLNGKWTANSVLEPGNSE 300
DB 241 ELBYIHILIEBRLVREHLTNHLKSKEVWKLLOEMPLTALLRLNGKWTANSVLEPGNSE 300

QY 301 VSLVCEKLCNEKLLKKARIHPPHILIALETYKTGHGRGKLMRPDEBILKALDAAFYKT 360
DB 301 VSLVCEKLCNEKLLKKARIHPPHILIALETYKTGHGRGKLMRPDEBILKALDAAFYKT 360

QY 361 FKTVEPTGKRFLLADV SASMNQVLSILNASTVAAMCMVVTREKDSYVAFSDENV 420
DB 361 FKTVEPTGKRFLLADV SASMNQVLSILNASTVAAMCMVVTREKDSYVAFSDENV 420

QY 421 PCPYTDMTLOQVLMANSQIPAGGTDCLPMIWAOKNTTPADVFI VFTDNETPAGGVHRA 480
DB 421 PCPYTDMTLOQVLMANSQIPAGGTDCLPMIWAOKNTTPADVFI VFTDNETPAGGVHRA 480

QY 481 IALREYRKMDIPAKLIVCGMTSNGFTIADPDDRGMLDMCGFDTGALD 528
DB 481 IALREYRKMDIPAKLIVCGMTSNGFTIADPDDRGMLDMCGFDTGALD 528

RESULT 3
Q86WLJ3 HUMAN PRELIMINARY; PRT; 534 AA.
ID Q86WLJ3 HUMAN PRELIMINARY; PRT; 534 AA.
AC Q86WLJ3
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Gastric cancer multi-drug resistance protein variant.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
NCBI_TaxID=9606;
RN NUCLEOTIDE SEQUENCE.
RP Han Q., Wang X., Shi Y., Ding J., Fan D.;
RA Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY205315; AA047002.1; -; mRNA.
DR GO; GO:0030529; C:ribonucleoprotein complex; IEA.
DR InterPro; IPR008588; TR0VE.
DR Pfam; PF05731; TR0VE; 1.
DR PROSITE; PS50988; TR0VE; 1.
SQ SEQUENCE 534 AA; 60197 MW; 63A4B96A77B6DD2D CRC64;

Query Match 98.0%; Score 2732; DB 2; Length 534;
Best Local Similarity 99.6%; Pred. No. 1e-174;
Matches 526; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MESSVNQOPLNEKQIANSODGYVQVTDNMRLHRLFLCGSEGGTYIYKEQKLGLENBA 60
DB 1 MESSVNQOPLNEKQIANSODGYVQVTDNMRLHRLFLCGSEGGTYIYKEQKLGLENBA 60

QY 61 LIRLIEDRGCEVIOEIKSFQSEGRITTKOEPMLFALAI CSQCSDISTKQAFKAVSEVCR 120
DB 61 LIRLIEDRGCEVIOEIKSFQSEGRITTKOEPMLFALAI CSQCSDISTKQAFKAVSEVCR 120

QY 121 IPTHLFTFIQPKODKESMKCGMWRALRAIADWYNEKGMALALAVTKYKQRNGWSHK 180
DB 121 IPTHLFTFIQPKODKESMKCGMWRALRAIADWYNEKGMALALAVTKYKQRNGWSHK 180

QY 181 DLRLSHLKSSSEGLAVTKYITKGMEVHELYEKKALSVETELKYLEAVEKVKTRD 240
DB 181 DLRLSHLKSSSEGLAVTKYITKGMEVHELYEKKALSVETELKYLEAVEKVKTRD 240

QY 241 ELBYIHILIEBRLVREHLTNHLKSKEVWKLLOEMPLTALLRLNGKWTANSVLEPGNSE 300
DB 241 ELBYIHILIEBRLVREHLTNHLKSKEVWKLLOEMPLTALLRLNGKWTANSVLEPGNSE 300

QY 301 VSLVCEKLCNEKLLKKARIHPPHILIALETYKTGHGRGKLMRPDEBILKALDAAFYKT 360
DB 301 VSLVCEKLCNEKLLKKARIHPPHILIALETYKTGHGRGKLMRPDEBILKALDAAFYKT 360

QY 361 FKTVEPTGKRFLLADV SASMNQVLSILNASTVAAMCMVVTREKDSYVAFSDENV 420
DB 361 FKTVEPTGKRFLLADV SASMNQVLSILNASTVAAMCMVVTREKDSYVAFSDENV 420

QY 421 PCPYTDMTLOQVLMANSQIPAGGTDCLPMIWAOKNTTPADVFI VFTDNETPAGGVHRA 480
DB 421 PCPYTDMTLOQVLMANSQIPAGGTDCLPMIWAOKNTTPADVFI VFTDNETPAGGVHRA 480

QY 481 IALREYRKMDIPAKLIVCGMTSNGFTIADPDDRGMLDMCGFDTGALD 528
DB 481 IALREYRKMDIPAKLIVCGMTSNGFTIADPDDRGMLDMCGFDTGALD 528

RESULT 4
Q8LJAO HUMAN PRELIMINARY; PRT; 525 AA.
ID Q8LJAO HUMAN PRELIMINARY; PRT; 525 AA.
AC Q8LJAO
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Sjogren syndrome antigen A2 (60kDa, ribonucleoprotein autoantigen SS-A/Ro).
GN Name=SSA2; ORFNames=RP11-101B13.3-006;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
NCBI_TaxID=9606;
RN NUCLEOTIDE SEQUENCE.
RP Whitehead S.;
RA Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL136370; CA110822.1; -; Genomic DNA.
DR GO; GO:0030529; C:ribonucleoprotein complex; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR Ribonucleoprotein; Viral nucleoprotein.
SQ SEQUENCE 525 AA; 59269 MW; 9240B125E1038544 CRC64;

Query Match 95.4%; Score 2659; DB 2; Length 525;
Best Local Similarity 99.4%; Pred. No. 7.9e-170;
Matches 513; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MESSVNQOPLNEKQIANSODGYVQVTDNMRLHRLFLCGSEGGTYIYKEQKLGLENBA 60
DB 1 MESSVNQOPLNEKQIANSODGYVQVTDNMRLHRLFLCGSEGGTYIYKEQKLGLENBA 60

QY 61 LIRLIEDRGCEVIOEIKSFQSEGRITTKOEPMLFALAI CSQCSDISTKQAFKAVSEVCR 120
DB 61 LIRLIEDRGCEVIOEIKSFQSEGRITTKOEPMLFALAI CSQCSDISTKQAFKAVSEVCR 120

QY 121 IPTHLFTFIQPKODKESMKCGMWRALRAIADWYNEKGMALALAVTKYKQRNGWSHK 180
DB 121 IPTHLFTFIQPKODKESMKCGMWRALRAIADWYNEKGMALALAVTKYKQRNGWSHK 180

QY	181	DLLRISHKPSSEGLAIYTKYITKGMKEVHELYPEKALSVETBKLLKTYLBAVEKVRKTD	240
Db	181	DLRLSHLKPSSEGLAIYTKYITKGMKEVHELYPEKALSVETBKLLKTYLBAVEKVRKTD	240
QY	241	ELEVHHLIEEHRLVBEHLLTNHLKKEVWKALLOEMPLFALLRNLGKMTANSLBEGNSE	300
Db	241	ELEVHHLIEEHRLVBEHLLTNHLKKEVWKALLOEMPLFALLRNLGKMTANSLBEGNSE	300
QY	301	VSIVCEKLCNEKLLKKARIRHPHILIALETTYTGHLRGKLLKMRPDEILIKALDAFYKT	360
Db	301	VSIVCEKLCNEKLLKKARIRHPHILIALETTYTGHLRGKLLKMRPDEILIKALDAFYKT	360
QY	361	FKTVEPTGRFLAVDVASAMNQRYLGSILNASTYAAMAMVYTRTEKDSYVAFSEDMV	420
Db	361	FKTVEPTGRFLAVDVASAMNQRYLGSILNASTYAAMAMVYTRTEKDSYVAFSEDMV	420
QY	421	PCPYTTDMTLQOVLAMSGIIPAGGIDCSIPMIWAOKTNPADVFIYFTDNEFPAGGVHPA	480
Db	421	PCPYTTDMTLQOVLAMSGIIPAGGIDCSIPMIWAOKTNPADVFIYFTDNEFPAGGVHPA	480
QY	481	IALREYRKMDIPAKLIVCGMTSNGTTADPPDRGM	516
Db	481	IALREYRKMDIPAKLIVCGMTSNGTTADPPDRGM	516

	RESULT 5			
Q5LJ98_HUMAN	518 AA.	PRT;		
ID Q5LJ98_HUMAN PRELIMINARY;				
AC Q5LJ98;				
DT 01-FEB-2005 (TREMBLrel. 29, Created)				
DT 01-FEB-2005 (TREMBLrel. 29, Last sequence update)				
DT 01-FEB-2005 (TREMBLrel. 29, Last annotation update)				
DE Sjogren syndrome antigen A2 [60kDa, ribonucleoprotein autoantigen SS-A/Ro].				
DZ GN Name=SSA2; ORFNames=RP11-101E13.3-003;				
OS Homo sapiens (Human).				
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;				
OC Homo.				
OX NCBI_TaxID=9606;				
RN [1]				
RP NUCLEOTIDE SEQUENCE.				
RA Whitehead S.;				
RL Submitted (May-2005) to the EMBL/Genbank/DBJ databases.				
DR EMBL; AL136370; CAIL0824.1; -; Genomic DNA.				
DR GO; GO:0030529; C:ribonucleoprotein complex; IEA.				
DR GO; GO:0004618; F:phosphoglycerate kinase activity; IEA.				
DR GO; GO:0003723; F:RNA binding; IEA.				
DR GO; GO:0006096; P:glycolysis; IEA.				
DR InterPro; IPR001576; PGK.				
DR InterPro; IPR008858; TROVE.				
DR Pfam; PF05731; TROVE; 1.				
DR PROSITE; PS00988; TROVE; 1.				
KW Ribonucleoprotein; Viral nucleoprotein.				
KW SEQUENCE 518 AA; 58483 MW; DCESS50ADBB261B CRC64;				
Query Match	95.3%;	Score 2657;	DB 2;	Length 518;
Best Local Similarity	99.8%;	Pred. No. 1.1e-169;		
Matches 513; Conservative 1;	Mismatches 0;	Indels 0;	Gaps 0;	
QY 1 MEESVNGQPANKEQIANSGGTYWGVTDMNRHRLFCSGGEGYYIKEDKLGENEA 60				
Db 1 MEESVNQNPINERKQIANSDGYWQVTDNMRLHLFLCFSGEGGYYIKEDKLGENEA 60				
QY 61 LIRLIEDRGGEVIOETKSFSOEGRTTKOEPLPALAI CSQCSDISTKQAAPKAIVSEVC 120				
Db 61 LIRLIEDRGGEVIOETKSF SOEGRTTKOEPLPALAISCSQSDISTKQAPKAIVSEVC 120				
QY 121 IPTLLFTTIQPKDKLKESMKGMGRALRKAIADVYNKGGMALATAATKYTKORNGSMHK 180				
Db 121 IPTLLFTTIQPKDKLKESMKGMGRALRKAIADVYNKGGMALATAATKYTKORNGSMHK 180				

QY	161	DLRLSLHKPSSEGLAIYKXITGTMKEVHELYERKALSVETEKLLKYLAEAEKVRTD	240
Db	181	DLRLSLHKPSSEGLAIYKXITGTMKEVHELYERKALSVETEKLLKYLAEAEKVRTD	240
QY	241	ELEVIHLIEERLYAEHLITYNHLSKEVWKALLOEMPLTALLRNIGKMTANSVLEBGNB	300
Db	241	ELEVIHLIEERLYAEHLITYNHLSKEVWKALLOEMPLTALLRNIGKMTANSVLEBGNB	300
QY	301	VSIVCEKLCNEKLLKKARIRHPHILIALETYKTGHGRKLMRPDEILKALDAAFYKT	360
Db	301	VSIVCEKLCNEKLLKKARIRHPHILIALETYKTGHGRKLMRPDEILKALDAAFYKT	360
QY	361	FKTVEPTGKRFLLAVDVASAMNQRVLSIINASTYAAAMCMVVTRETKOSYVAFSDEVY	420
Db	361	FKTVEPTGKRFLLAVDVASAMNQRVLSIINASTYAAAMCMVVTRETKOSYVAFSDEVY	420
QY	421	PCPVTTMTLQOYVLMASQIPAGGVDGSLPMIWAQKTPADPVFIYFTDNETPAGGVHRA	480
Db	421	PCPVTTMTLQOYVLMASQIPAGGVDGSLPMIWAQKTPADPVFIYFTDNETPAGGVHRA	480
QY	481	IALREYRKQMDIPAKLIVCGMTNSGFTIADPPDR	514
Db	481	IALREYRKQMDIPAKLIVCGMTNSGFTIADPPDR	514

RESULT 6	086M14 HUMAN	086M14_HUMAN PRELIMINARY;	PRT;	518 AA.
ID	086M14			
AC	086M14			
DT	01-JUN-2003 (TREMBLrel. 24, Created)			
DT	01-JUN-2003 (TREMBLrel. 24, Last sequence update)			
DT	01-MAR-2004 (TREMBLrel. 26, Last annotation update)			
DE	Gastric cancer multi-drug resistance protein variant.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi;			
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;			
OC	Homo.			
OX	NCBI_Taxid=9606;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE.			
RA	Han Q., Wang X., Shi Y., Ding J., Fan D.,			
RL	Submitted (DEC-2002) to the EMBL/Genbank/DBJ databases.			
DR	EMBL; AY205314; AAC47001.1; -, mRNA.			
DR	GO; GO:0030529; C:ribonucleoprotein complex; IEA.			
DR	GO; GO:0003723; F:RNA binding; IEA.			
DR	InterPro; IPR006858; TROVE.			
DR	Pfam; PF05731; TROVE, 1.			
DR	PROSITE; PS50988; TROVE, 1.			
SO	SEQUENCE 518 AA; 58511 MW; 42C3508D26385A1 CRC64;			
Query Match	95.2%; Score 2654; DB 2; Length 518;			
Best Local Similarity	99.6%; Pred. No. 1.7e-169;			
Matches 512; Conservative	2; Mismatches 0; Indels 0; Gaps 0;			
QY	1 MESSVQWQPIINERKQIANSODGYVQVTDNRRILRFLCFSGSEGYYIKKQKLGLENAA 60			
DB	1 MESSVQWQPIINERKQIANSODGYVQVTDNRRILRFLCFSGSEGYYIKKQKLGLENAA 60			
QY	61 LIRLIDEGRGCEVIOETKSPQBERTTKQEMFLALAI CQCGSISITKQAFKAVSEVCR 120			
DB	61 LIRLIDEGRGCEVIOETKSPQBERTTKQEMFLALAI CQCGSISITKQAFKAVSEVCR 120			
QY	121 IPTHLPFIQKQDLRESMKCGMGRALRKRLADVYNEKGMALALAVTKYKORNGWSHK 180			
DB	121 IPTHLPFIQKQDLRESMKCGMGRALRKRLADVYNEKGMALALAVTKYKORNGWSHK 180			
QY	181 DLRLSLKPSSEGIAIVTKIITGKWEVHELVEKALSVETKLLKYLEAVEKVRTYD 240			
DB	181 DLRLSLKPSSEGIAIVTKIITGKWEVHELVEKALSVETKLLKYLEAVEKVRTYD 240			
QY	241 ELVETIHLIEERLVRHLLTNHLKSKVWKLQDMPLTALLRLNGRTANSVLEPGNSE 300			
DB	241 ELVETIHLIEERLVRHLLTNHLKSKVWKLQDMPLTALLRLNGRTANSVLEPGNSE 300			
QY	300 ELVETIHLIEERLVRHLLTNHLKSKVWKLQDMPLTALLRLNGRTANSVLEPGNSE 300			
DB	300 ELVETIHLIEERLVRHLLTNHLKSKVWKLQDMPLTALLRLNGRTANSVLEPGNSE 300			

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QY 301 VSLVCEKLNCKEKLKKARIPHPHLLALETYKTHGRLGKLRPDEEILKALDAAPYKT 360
DB 301 VSLVCEKLNCKEKLKKARIPHPHLLALETYKTHGRLGKLRPDEEILKALDAAPYKT 360
QY 361 FKTYEPTGKRFLLAVDVASASNNQVLSIINASTVAAMCMVVRTEKDSYVAFSDMV 420
DB 361 FKTYEPTGKRFLLAVDVASASNNQVLSIINASTVAAMCMVVRTEKDSYVAFSDMV 420
QY 421 PCPVTDMTLQOVLMANSQIPAGGTDCLPMIWAQKNTVPADVIFVTDNETFAGVHPA 480
DB 421 PCPVTDMTLQOVLMANSQIPAGGTDCLPMIWAQKNTVPADVIFVTDNETFAGVHPA 480
QY 481 IALREYRKQMDIPAKLIYCGMTSNGFTIADPDDR 514
DB 481 IALREYRKQMDIPAKLIYCGMTSNGFTIADPDDR 514

RESULT 7
RO60_MOUSE STANDARD; PRT; 538 AA.
AC 008848; Q9QYD8;
DT 16-OCT-2001 (Ref. 40, Created)
DT 16-OCT-2001 (Ref. 40, Last sequence update)
DT 13-SEP-2005 (Ref. 48, Last annotation update)
DE 60-kDa S8-A/Ro ribonucleoprotein (60 kDa Ro protein) (60 kDa
ribonucleoprotein Ro) (RoRNP) (TROVE domain family member 2).
GN Name=Trove2; Synonyms=Saa2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN NUCLEOTIDE SEQUENCE.
RP TISUS-Heart;
RC MEDLINE=97266462; PubMed=9112230;
RA Wang D., Buyn J.P., Chan E.K.L.;
RT "Cloning and expression of mouse 60 kDa ribonucleoprotein S8-A/Ro.";
RL Mol. Biol. Rep. 23:205-210(1996).
[2]
RN NUCLEOTIDE SEQUENCE.
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=129/SvJ;
RA PubMed=11196703; DOI=10.1038/ej.gene.6363675;
RA Kaufman K.M., Farria A.D., Gross J.K., Kirby M.Y., Harley J.B.;
RT "Characterization and genomic sequence of the murine 60 kD Ro gene.";
RL Genes Immun. 1:265-270(2000).
[3]
RN NUCLEOTIDE SEQUENCE OF 82-538.
RP MEDLINE=99255038; PubMed=10323459;
RX DOI=10.1002/1529-0131(199905)42:5<1017::AID-ANR22>3.0.CO;2-7;
RA Scofield R.H., Kaufman K.M., Baber U., James J.A., Harley J.B.,
Kurtien B.T.;
RT "Immunization of mice with human 60-kD Ro peptides results in epitope
spreading if the peptides are highly homologous between human and
mouse.";
RL Arthritis Rheum. 42:1017-1024(1999).
RN NUCLEOTIDE SEQUENCE.
RP NUCLEOTIDE SEQUENCE.
RC CYCLOPLASMIC RNA molecules known as Y RNAs. May stabilize these
RNAs from degradation.
RA SUBUNIT: Binds RPL1 (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- TISSUE SPECIFICITY: Highest in brain, followed by lung, muscle,
CC kidney and heart. Lower levels are found in testis, liver and
CC spleen.
CC -1- SIMILARITY: Belongs to the Ro 60 kDa family.
CC -1- SIMILARITY: Contains 1 TROVE domain.
CC This Swiss-Prot entry is copyrighted. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.

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CC -----
DR EMBL: U66843; AAC53142.1; -, mRNA.
DR EMBL: AF065398; AAF19049.1; -, Genomic DNA.
DR EMBL: AF042139; AAC15667.1; -, Genomic DNA.
DR Ensemble: ENSMUSG00000018199; Mus musculus.
DR MGI: MGI:106652; Saa2.
DR InterPro: IPR008858; TROVE.
DR Pfam: PF05731; TROVE; 1.
DR PROSITE: PS50988; TROVE; 1.
KW Ribonucleoprotein; RNA-binding.
FT DOMAIN 16 369 TROVE.
FT CONFLICT 32 33 RL -> V (in Ref. 2).
FT CONFLICT 458 458 D -> G (in Ref. 2).
FT CONFLICT 465 465 V -> I (in Ref. 2).
SQ SEQUENCE 538 AA; 60124 MW; 7850DA35D1726BDA CRC64;

Query Match 91.2%; Score 2541; DB 1; Length 538;
Best Local Similarity 90.0%; Pred. No. 6,7e-162;
Matches 484; Conservative 29; Mismatches 25; Indels 0; Gaps 0;

QY 1 MESSVNMOPLINEKOIANSQDGYVVOYTDNMRHLRFLCFSGEGGTYIIKEOKLLENAA 60
DB 1 MESSANQIQLSTQVNVNSBGCVMQVTDNMRHLRFLCFSGEGGTYIIKEOKLLENAA 60
QY 61 LIRLIEDRGCEVIOETKSFSGEGRTTKOEPMLPALAICQCSDSITKQAAFKAVSEYCR 120
DB 61 LIRLIEDRGCEVIOETKSFSGEGRTTKOEPMLPALAICQCSDSITKQAAFKAVSEYCR 120
QY 61 LIRLIEDRGCEVIOETKSFSGEGRTTKOEPMLPALAICQCSDSITKQAAFKAVSEYCR 120
DB 61 LIRLIEDRGCEVIOETKSFSGEGRTTKOEPMLPALAICQCSDSITKQAAFKAVSEYCR 120
QY 121 IPTHLFTPIQPKOLKESMKCGMGRALRKAIADWYNEKGMALAVTKKQNGSHK 180
DB 121 IPTHLFTPIQPKOLKESMKCGMGRALRKAIADWYNEKGMALAVTKKQNGSHK 180
QY 121 IPTHLFTPIQPKOLKESMKCGMGRALRKAIADWYNEKGMALAVTKKQNGSHK 180
DB 121 IPTHLFTPIQPKOLKESMKCGMGRALRKAIADWYNEKGMALAVTKKQNGSHK 180
QY 181 DLRLSHLRPSSEGLAVTKYITGWMKEVHELYEKSLVETELKTLBAVEKYRTKD 240
DB 181 DLRLSHLRPSSEGLAVTKYITGWMKEVHELYEKSLVETELKTLBAVEKYRTKD 240
QY 181 DLRLSHLRPSSEGLAVTKYITGWMKEVHELYEKSLVETELKTLBAVEKYRTKD 240
DB 181 DLRLSHLRPSSEGLAVTKYITGWMKEVHELYEKSLVETELKTLBAVEKYRTKD 240
QY 241 ELEVIHLIEHRILVREHLITNHLKSKYWKALQEMPLTALLRNIGKVTANSVLEPNSG 300
DB 241 ELEVIHLIEHRILVREHLITNHLKSKYWKALQEMPLTALLRNIGKVTANSVLEPNSG 300
QY 241 ELEVIHLIEHRILVREHLITNHLKSKYWKALQEMPLTALLRNIGKVTANSVLEPNSG 300
DB 241 ELEVIHLIEHRILVREHLITNHLKSKYWKALQEMPLTALLRNIGKVTANSVLEPNSG 300
QY 301 VSLVCEKLNCKEKLKKARIPHPHLLALETYKTHGRLGKLRPDEEILKALDAAPYKT 360
DB 301 VSLVCEKLNCKEKLKKARIPHPHLLALETYKTHGRLGKLRPDEEILKALDAAPYKT 360
QY 301 VSLVCEKLNCKEKLKKARIPHPHLLALETYKTHGRLGKLRPDEEILKALDAAPYKT 360
DB 301 VSLVCEKLNCKEKLKKARIPHPHLLALETYKTHGRLGKLRPDEEILKALDAAPYKT 360
QY 361 FKTYEPTGKRFLLAVDVASASNNQVLSIINASTVAAMCMVVRTEKDSYVAFSDMV 420
DB 361 FKTYEPTGKRFLLAVDVASASNNQVLSIINASTVAAMCMVVRTEKDSYVAFSDMV 420
QY 361 FKTYEPTGKRFLLAVDVASASNNQVLSIINASTVAAMCMVVRTEKDSYVAFSDMV 420
DB 361 FKTYEPTGKRFLLAVDVASASNNQVLSIINASTVAAMCMVVRTEKDSYVAFSDMV 420
QY 421 PCPVTDMTLQOVLMANSQIPAGGTDCLPMIWAQKNTVPADVIFVTDNETFAGVHPA 480
DB 421 PCPVTDMTLQOVLMANSQIPAGGTDCLPMIWAQKNTVPADVIFVTDNETFAGVHPA 480
QY 421 PCPVTDMTLQOVLMANSQIPAGGTDCLPMIWAQKNTVPADVIFVTDNETFAGVHPA 480
DB 421 PCPVTDMTLQOVLMANSQIPAGGTDCLPMIWAQKNTVPADVIFVTDNETFAGVHPA 480
QY 481 IALREYRKQMDIPAKLIYCGMTSNGFTIADPDDRGMDCGFDGALDIVIRNFTLMT 538
DB 481 IALREYRKQMDIPAKLIYCGMTSNGFTIADPDDRGMDCGFDGALDIVIRNFTLMT 538
QY 481 IALREYRKQMDIPAKLIYCGMTSNGFTIADPDDRGMDCGFDGALDIVIRNFTLMT 538
DB 481 IALREYRKQMDIPAKLIYCGMTSNGFTIADPDDRGMDCGFDGALDIVIRNFTLMT 538

RESULT 8
Q8R562_MOUSE PRELIMINARY; PRT; 538 AA.
AC 08R562;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Ribonucleoprotein.
GN Name=Saa2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN NUCLEOTIDE SEQUENCE.
RP NUCLEOTIDE SEQUENCE.

```

RA Kamepelli C.C., Fu S.M.;
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; L61154; ALU7518.1; -, mRNA.
 DR MGI; MGI:106652; Ssa2.
 DR GO; GO:0030529; Citronucleoprotein complex; IEA.
 DR GO; GO:0003723; F:RNA binding; IEA.
 DR InterPro; IPR008858; TROVE.
 DR Pfam; PF05731; TROVE; 1.
 DR PROSITE; PS50988; TROVE; 1.
 KW Ribonucleoprotein.
 SQ SEQUENCE 538 AA; 60153 MW; 65E46C843FA4572E CRC64;
 Query Match 91.0%; Score 2535; DB 2; Length 538;
 Best Local Similarity 89.8%; Pred. No. 1,7e-161;
 Matches 483; Conservative 29; Mismatches 26; Indels 0; Gaps 0;
 QY 1 MBSVNMQPLNEKQIANSODGYVQVDTMNRHLRFICSGSEGCTYYIKQKLGLENAA 60
 DB 1 MEGSANQLOPLSETQVNVSEGGCVQVDTMNRRLRRLFCFSGEGTYYIKQKLGLENAA 60
 QY LRLRLIDGRCCEVIOEIKFSQSGRTTKORPMLFALATGSCSDISTKQAAFAVSEVCR 120
 DB LRLRLIDGRCCEVIOEIKFSQSGRTAKOEPFLFALAVCSQCADINTKQAAFAVSEVCR 120
 QY 121 IPTHLETFIOFKKDLKESMKCGMGRALKRAIADWYNEKGMALALAVTKYKQRNGMSHK 180
 DB 121 IPTHLETFIOFKKDLKESMKCGMGRALKRAVADWYNEKGMALVALVTKYKQRNGMSHK 180
 QY 121 IPTHLETFIOFKKDLKESMKCGMGRALKRAVADWYNEKGMALVALVTKYKQRNGMSHK 180
 DB 121 IPTHLETFIOFKKDLKESMKCGMGRALKRAVADWYNEKGMALVALVTKYKQRNGMSHK 180
 QY 181 DLRLSHLKPSSEGLAIVTKYITKGWKEVHELYEKALSVETEKLYLEAVEKVKRTKD 240
 DB 181 DLRLSHLKPSSEGLAIVTKYITKGWKEVHELYEKALSVETEKLYLEAVEKVKRTKD 240
 QY 241 ELEVTHLIEBHRLVREHLLTNHLKSKVWKALLOEMPLTALLNLGKMTANSVLEPGNSE 300
 DB 241 ELEVTHLIEBHRLVREHLLTNHLKSKVWKALLOEMPLTALLNLGKMTANSVLEPGNSE 300
 QY 301 VSLVCEKLCNEKLLKTKARLHPHILLALETKYTGHLRGRLKMRPDEELIKALDAAFYKT 360
 DB 301 VSLVCEKLSNEKLLKTKARLHPHILLALETKYTGHLRGRLKMRPDEELIKALDAAFYKT 360
 QY 361 FKTVEPTGKRFLLADVVSANMQRVLGSIINASTVAAAMCMVTRTEKSSVVAFAFCDW 420
 DB 361 FKTVEPTGKRFLLADVVSANMQRVLGSIINASTVAAAMCMVTRTEKSSVVAFAFCDW 420
 QY 421 PCVTDTMTLQOVLAMNSOIPAGTDCSLPMIWAQKNTPADVFYFTDNETFAGGVHRA 480
 DB 421 PCVTDTMTLQOVLAMNSOIPAGTDCSLPMIWAQKNTPADVFYFTDNETFAGGVHRA 480
 QY 481 IALREYRKMDIPAKLIVCGMTSNGFTIADPDRGMLDMCGPDTGALDVIKNTFLDMI 538
 DB 481 VALREYRKMDIPAKLIVCGMTSNGFTIADPDRGMLDMCGPDTGALDVIKNTFLDMI 538
 RESULT 9
 ID 080M12 MOUSE PRELIMINARY; PRT; 538 AA.
 AC 080M12;
 DT 01-JUN-2003 (T-EMBLrel. 24, Created)
 DT 01-JUN-2003 (T-EMBLrel. 24, Last sequence update)
 DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
 DE 60KD Ro/SSA autoantigen.
 GN Name=Ssa2;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse S.J., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Alteschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
 RA Brownstein M.U., Ustin T.B., Toshiyuki S., Carninci P., Prange C.J.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richarad S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RP [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RA Strausberg R.;
 RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC051974; AAH51974.1; -, mRNA.
 DR MGI; MGI:106652; Ssa2.
 DR GO; GO:0030529; Citronucleoprotein complex; IEA.
 DR GO; GO:0003723; F:RNA binding; IEA.
 DR InterPro; IPR008858; TROVE.
 DR Pfam; PF05731; TROVE; 1.
 DR PROSITE; PS50988; TROVE; 1.
 SQ SEQUENCE 538 AA; 60171 MW; 7850C6E41C726BDA CRC64;
 Query Match 90.9%; Score 2532; DB 2; Length 538;
 Best Local Similarity 89.8%; Pred. No. 2,7e-161;
 Matches 483; Conservative 29; Mismatches 26; Indels 0; Gaps 0;
 QY 1 MBSVNMQPLNEKQIANSODGYVQVDTMNRHLRFICSGSEGCTYYIKQKLGLENAA 60
 DB 1 MEGSANQLOPLSETQVNVSEGGCVQVDTMNRRLRRLFCFSGEGTYYIKQKLGLENAA 60
 QY LRLRLIDGRCCEVIOEIKFSQSGRTTKORPMLFALATGSCSDISTKQAAFAVSEVCR 120
 DB LRLRLIDGRCCEVIOEIKFSQSGRTAKOEPFLFALAVCSQCADINTKQAAFAVSEVCR 120
 QY 121 IPTHLETFIOFKKDLKESMKCGMGRALKRAIADWYNEKGMALALAVTKYKQRNGMSHK 180
 DB 121 IPTHLETFIOFKKDLKESMKCGMGRALKRAVADWYNEKGMALVALVTKYKQRNGMSHK 180
 QY 121 IPTHLETFIOFKKDLKESMKCGMGRALKRAVADWYNEKGMALVALVTKYKQRNGMSHK 180
 DB 121 IPTHLETFIOFKKDLKESMKCGMGRALKRAVADWYNEKGMALVALVTKYKQRNGMSHK 180
 QY 181 DLRLSHLKPSSEGLAIVTKYITKGWKEVHELYEKALSVETEKLYLEAVEKVKRTKD 240
 DB 181 DLRLSHLKPSSEGLAIVTKYITKGWKEVHELYEKALSVETEKLYLEAVEKVKRTKD 240
 QY 241 ELEVTHLIEBHRLVREHLLTNHLKSKVWKALLOEMPLTALLNLGKMTANSVLEPGNSE 300
 DB 241 ELEVTHLIEBHRLVREHLLTNHLKSKVWKALLOEMPLTALLNLGKMTANSVLEPGNSE 300
 QY 301 VSLVCEKLCNEKLLKTKARLHPHILLALETKYTGHLRGRLKMRPDEELIKALDAAFYKT 360
 DB 301 VSLVCEKLSNEKLLKTKARLHPHILLALETKYTGHLRGRLKMRPDEELIKALDAAFYKT 360
 QY 361 FKTVEPTGKRFLLADVVSANMQRVLGSIINASTVAAAMCMVTRTEKSSVVAFAFCDW 420
 DB 361 FKTVEPTGKRFLLADVVSANMQRVLGSIINASTVAAAMCMVTRTEKSSVVAFAFCDW 420
 QY 421 PCVTDTMTLQOVLAMNSOIPAGTDCSLPMIWAQKNTPADVFYFTDNETFAGGVHRA 480
 DB 421 PCVTDTMTLQOVLAMNSOIPAGTDCSLPMIWAQKNTPADVFYFTDNETFAGGVHRA 480
 QY 481 IALREYRKMDIPAKLIVCGMTSNGFTIADPDRGMLDMCGPDTGALDVIKNTFLDMI 538
 DB 481 VALREYRKMDIPAKLIVCGMTSNGFTIADPDRGMLDMCGPDTGALDVIKNTFLDMI 538

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RESULT 10
Q7TT40_MOUSE PRELIMINARY; PRT; 547 AA.
ID Q7TT40_MOUSE PRELIMINARY; PRT; 547 AA.
AC Q7TT40_MOUSE PRELIMINARY; PRT; 547 AA.
DT 01-OCT-2003 (T-EMBLrel. 25, Created)
DT 01-OCT-2003 (T-EMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE Name=8aa2;
GN Sea2 protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
NCBI_TaxID=10090;
OX
OC
NCBI_TaxID=10090;
[1]
RP NUCLEOTIDE SEQUENCE.
RP STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603699;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
RA Diatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedl T.B., Tomihata S., Carninci P., Prange C.,
RA Rha S.S., Loughran N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulys S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitling M., Madan A., Young A.C., Shevchenko Y., Boulford G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butlerfield Y.S.N., Krzywinski M.I., Skelton U., Smallie D.E.,
RA Scheraga A., Schell J.B., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RP NUCLEOTIDE SEQUENCE.
RP STRAIN=C57BL/6; TISSUE=Brain;
RX Strausberg R.,
RA Submitted (May-2003) to the EMBL/GenBank/DBJ databases.
RL EMBL, BC052380; AAH52380.1; -; mRNA.
DR GO, GO:0030529; C:ribonucleoprotein complex; IEA.
DR GO, GO:0003723; F:RNA binding; IEA.
DR InterPro, IPR008658; TROVE.
DR PROSITE, PS50988; TROVE, 1.
FT NON TER
SQ SEQUENCE 547 AA; 61272 MW; 2CF235A0C803510F CRC64;
Query Match 90.9%; Score 2532; DB 2; Length 547;
Best Local Similarity 89.8%; Pred. No. 2.7e-151;
Matches 483; Conservative 29; Mismatches 26; Indels 0; Gaps 0;
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DB 250 DLEVIHLIEBQVLVREHLITNHLKSKVWALLQEMPTALLRNIGKMTANSVLEBGNSE 309
QY 301 VSLVCEKLNCKELKKARLHPHILLALFTYKTHGRLGKLRPDEILKALDAAPYKT 360
DB 310 VSLICEKLSNEKLLKARLHPHILLALFTYKTHGRLGKLRPDEILKALDAAPYKT 369
QY 361 FKTVEPTGKRFLLAVSVASMNORVLGSIINASTVAAACMVVTRTEKDSYVAFSDENV 420
DB 370 FKTVEPTGKRFLLAVSVASMNORVLGSIINASTVAAACMVVTRTEKDSYVAFSDENV 429
QY 421 PCFVTTDMTLQVLTAMASQIPAGTDCSLPMIWAQKNTPADVFIYFTDNETAGVHPA 480
DB 430 PFPVTTDMTLQVLTAMASQIPAGTDCSLPMIWAQKNTPADVFIYFTDNETAGVHPA 489
QY 481 IALREYRKAMDIPAKLIVCGMTSGFTIADPPDRGMLDMCGPRTGALDVIRNFTLDMI 538
DB 490 VALREYRKAMDIPAKLIVCGMTSGFTIADPPDRGMLDMCGPRTGALDVIRNFTLDMI 547
RESULT 11
RO60_XENLA STANDARD; PRT; 538 AA.
ID RO60_XENLA STANDARD; PRT; 538 AA.
AC P42700;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE 60-kDa SS-A/Ro ribonucleoprotein (60 kDa Ro protein) (60 kDa
DE ribonucleoprotein Ro) (RoRNP) (TROVE domain family member 2).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;
OC Xenopodidae; Xenopus; Xenopus.
OX
OC
NCBI_TaxID=8355;
[1]
RP NUCLEOTIDE SEQUENCE.
RP TISSUE=Embryo, and Ovary;
RX MEDLINE=93348251; PubMed=7688474;
RA O'Brien C.A., Margelot K., Wolin S.L.;
RT "Xenopus Ro ribonucleoproteins: members of an evolutionarily conserved
RT class of cytoplasmic ribonucleoproteins."
RL Proc. Natl. Acad. Sci. U.S.A. 90:7250-7254(1993).
CC -1- FUNCTION: RNA-binding protein that binds to several small
CC cytoplasmic RNA molecules known as Y RNAs. May stabilize these
CC RNAs from degradation.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: Belongs to the Ro 60 kDa family.
CC -1- SIMILARITY: Contains 1 TROVE domain.
-----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
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DR EMBL, L15430; AAC38001.1; -; mRNA.
DR PIR, I51560; I51560.
DR InterPro, IPR008858; TROVE.
DR Pfam, PF05731; TROVE, 1.
DR PROSITE, PS50988; TROVE, 1.
FT Ribonucleoprotein; RNA-binding.
FT DOMAIN 16 369 TROVE.
SQ SEQUENCE 538 AA; 60688 MW; 548C17B0AE9BBD6 CRC64;
Query Match 81.4%; Score 2269; DB 1; Length 538;
Best Local Similarity 78.6%; Pred. No. 1.2e-143;
Matches 423; Conservative 59; Mismatches 56; Indels 0; Gaps 0;
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Db 61 LURLIDGKGEVVOEIKTPSGEGRABKOEPTLALAVCSQCSIDIKTKQAAPRAVEVCR 120
Qy 121 IPRHLFTIOPFKDKLKEKMGKMGWGRALKAIDVYNEKCGMALALAVTKYKORNGMSH 180
Db 121 IPRHLFTIOPFKDKLKEKMGKMGWGRALKAIDVYNEKCGMALALAVTKYKORNGMSH 180
Qy 181 DLLRLSHLKSSSEGLAVTKYTKGWKEVHELKYEKALSVETEKLLKYLEAVEKVKRTD 240
Db 181 DLLRLSHLKSSSEGLAVTKYTKGWKEVHELKYEKALSVETEKLLKYLEAVEKVKRTD 240
Qy 241 ELEVIHLIEBRLVREHLTLTNHLKSKVWVALLQEMPTALLRNIGKMTANSVLEPGNS 300
Db 241 ELEVIHLIEBRLVREHLTLTNHLKSKVWVALLQEMPTALLRNIGKMTANSVLEPGNS 300
Qy 301 VSLVCEKLCNEKLLKARLHPHILALETYKTHGKGRGLKRPDEEILKALDAAPYKT 360
Db 301 VSSVCEKLTNEKLLKARLHPHILALETYKTHGKGRGLKRPDEEILKALDAAPYKT 360
Qy 361 PKTVEPTGRPLAVVSAVSMNQRYLGSILNASTVAAMGVVTRTEKDSYVAFSDENV 420
Db 361 PKTVEPTGRPLAVVSAVSMNQRYLGSILNASTVAAMGVVTRTEKDSYVAFSDENV 420
Qy 421 PCFVTTDMTLQOVLAMASQIPAGTDCSLPMIAOKTNPADVFIYFTDNEPAGVHPA 480
Db 421 PCFVTTDMTLQOVLAMASQIPAGTDCSLPMIAOKTNPADVFIYFTDNEPAGVHPA 480
Qy 481 IALREPRKMDIPAKLIVCGMTSNGFTIADPPDRGMLDMCGPDTGALDVIRNTLDMI 538
Db 481 TALQYREKKGIPAKLIVCGMTSNGFTIADPPDRGMLDMCGPDTGALDVIRNTLDMI 538
RESULT 12
Q4SP44.TETNG
ID Q4SP44.TETNG PRELIMINARY; PRT; 547 AA.
AC Q4SP44.
DT 13-SEP-2005 (TEMBLrel. 31, Created)
DT 13-SEP-2005 (TEMBLrel. 31, Last sequence update)
DE 13-SEP-2005 (TEMBLrel. 31, Last annotation update)
Chromosome 15 SCAP14542, whole genome shotgun sequence.
GN ORFNames=GSTENG00014938001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99863;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Jallion O., Aury J.M., Brunet F., Petit J.L., Strange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Coetzar C., Bernot A.,
RA Nicard S., Jaffe D., Fisher S., Luttalla G., Dossat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA Blemont C., Skallis Z., Cattoiello L., Poulin J., De Berardinis V.,
RA Cunard C., Duprat S., Broctier P., Couanceau J.P., Gouy J.,
RA Parra G., Lardier G., Chapelle C., McKernan K.J., McMan P., Bosak S.,
RA Keilis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Wincker P., Lander E.S., Weissenbach J., Roest Crolius H.;
RA "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT the early vertebrate proto-karyotype";
RL Nature 431:946-957(2004).
[2]
RP NUCLEOTIDE SEQUENCE.
RG Genoscope, Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAE01014542; CAP97528.1; -; Genomic DNA.
SQ SEQUENCE 547 AA; 60290 MW; ED022BD11A3E727A CRC64;

Query Match 55.4%; Score 1544.5; DB 2; Length 547;
Best local similarity 53.0%; Pred. No. 4.6e-95;
Matches 290; Conservative 109; Mismatches 139; Indels 9; Gaps 4;
Qy 1 MEESVNOQPLNEKQIANSODGYVQVTDMLRHLRFLCGSGGGTYIYEOK-LGLENN 59
Db 1 MEPAVASAVPEENHHTWSATGGCCQMEVTDRLCEFLCYGGRHYVTAREEENLSQSG 60
Qy 60 ALIRLEDGRGGEVVOEIKTPSGEGRABKOEPTLALAVCSQCSIDIKTKQAAPRAVSEVC 119
Db 61 ALMSMLQEGRGABVVEIKKLAREGAVRPPSPFALALCSQHSILTKQAAPRAVSEVC 120
Qy 120 RIPLHLFTIOPFKDKLKEKMGKMGWGRALKAIDVYNEKCGMALALAVTKYKORNGMSH 179
Db 121 RPPAQLFAIIOKKELKEKMGKMGWGRALKAIDVYNEKCGMALALAVTKYKORNGMSH 180
Qy 180 KDLLRLSHLKSSSEGLAVTKYTKGWKEVHELKYEKALSVETEKLLKYLEAVEKVKRTK 239
Db 181 RDLLRLCHTKRPANEAIALICKYATKGMKEVQVAYANKENSEEVDRLSTYLEAVEKVMHC 240
Qy 240 DELEVIHLIEBRLVREHLTLTNHLKSKVWVALLQEMPTALLRNIGKMTANSVLEPGNS 299
Db 241 DELEVIHLIEBRLVREHLTLTNHLKSKVWVALLQEMPTALLRNIGKMTANSVLEPGNS 300
Qy 300 EVSLVCEKLCNEKLLKARLHPHILALETYKTHGKGRGLKRPDEEILKALDAAPYKT 360
Db 301 ETOAVGERIQCETALKKAGFOLKQARLHPHILALETYKTHGKGRGLKRPDEEILKAL 360
Qy 361 LDAAPYKTEKTYEPGRPLAVVSAVSMNQRYLGSILNASTVAAMGVVTRTEKDSYV 412
Db 361 MESAFYKSFVNVEPAGRRFPIVADVSTLSVPGTPISTALIAAIAAMFVTEADTEV 420
Qy 413 VAFSD-EMVPCFVTTDMTLQOVLAMASQIPAGTDCSLPMIAOKTNPADVFIYFTDNE 471
Db 421 LNVSEGVVPCAVTADMTLAEVTSVAVSGSDTCLVTVYATBEDRADVAVVLTNP 480
Qy 472 TRAGVHPAIALREYKKNMDIPAKLIVCGMTSNGFTIADPPDRGMLDMCGPDTGALDVIR 531
Db 481 LMPFSPAPLFTIQKRRKRGASSKVIVICGLTNSGSLADTBEDGGLSIGFDGALSVIR 540
Qy 532 NPTLDMI 538
Db 541 NLAQDLI 547
RESULT 13
Q5M7X5.BRARE
ID Q5M7X5.BRARE PRELIMINARY; PRT; 558 AA.
AC Q5M7X5.
DT 01-FEB-2005 (TEMBLrel. 29, Created)
DT 01-FEB-2005 (TEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TEMBLrel. 29, Last annotation update)
DE Hypothetical protein (Fragment).
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Whole;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Umedin T.B., Toshlyuk S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richard S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahy J., Halton E., Ketteman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Ruedenfeld Y.S.N., Krzywinski M.I., Skaleka U., Smallus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Maria M.A.,
 RT "generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE-whole.
 RA Director MGC Project;
 RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC088391; AAH8391.1; -, mRNA.
 DR GO; GO:0030529; C:ribonucleoprotein complex; IEA.
 DR GO; GO:0003723; F:RNA binding; IEA.
 DR InterPro; IPR008858; TROVE.
 DR Pfam; PF05731; TROVE; 1.
 DR PROSITE; PS50988; TROVE; 1.
 KM Hypothetical protein.
 FT NON TER
 SQ SEQUENCE 558 AA; 61579 MW; 92158A20E2406856 CRC64;
 Query Match 54.4%; Score 1517; DB 2; Length 558;
 Best Local Similarity 54.5%; Pred. No. 3.3e-93;
 Matches 290; Conservative 99; Mismatches 135; Indels 8; Gaps 5;
 QY 7 OMQPLNKQJANSODGYVQVTDNNRLHRLFCFSGSEGGTYIKKQKGLNVAALIRLIE 66
 DB 33 QLSVANE-QVANSADR---SVTAAVCLRRFLCYGSEBSSTYTKCPGLIGENALSLMOIIE 88
 QY 67 DGRCEVYIOEIKFSQSEGRITKQEPMLFALAICSCQSDISTKQAFKAVSEVCRIPHLF 126
 DB 89 GGRSEVVDYRRNRNLGSAVRPNPGLFTLAVCSQHADCKTRQALRALKELCSSPMQLF 148
 QY 127 TFIQPKDKESMKCGMGRALRKALADWYNEKGMALALAVTKYKQNGSHDILRLS 186
 DB 149 TPVQYKKEIKEG--SGMWGRALRRVVDWYNGODGISLAQAVTKCKRAKMGSHDILRLS 206
 QY 187 HIKRSSSGIALVTYKTKGKWEVHELVEKALSVTEKLLKYLAWEKVKTKQLEVIYI 246
 DB 207 HMKRPNNDIALVCKYITKGMGVEBANAEXKSDLEDLPAYLAEVKEVKASTDEBELIH 266
 QY 247 LIEBRLVREHLTNHLKSKVEWKALIQEMPLTALLRNIGKQNTANSVLEPNSSEVSLVCE 306
 DB 267 LIEFORLKGKOLLTNHLKSKVEWKALKEMPVAVLLKHLGLTNKVLIPGSPDLAIVCG 326
 QY 307 KLQNEKLKARIRHPHILALETYTGTHGRLGKLRPDEBILKALDAAYTKFYKTYEP 366
 DB 327 RIQRETVLKAKAKTQPFNIIAASENFKRGHGRSKLKWEPDLDVQALDCAKCSISTIEA 386
 QY 367 TGRKFLAVNDVASMNQVAVLSIINASTVVAAMCMVVRTRTKDSVVAFSP-EMVPCPYT 425
 DB 387 TGRKFLAVNDVSSISLSCRSSISSTVAVAACVILIAQTEPMQIVFSSGNLPLCTVS 446
 QY 426 TDMTIAQVILAMSGQIPAGTDCSLPIMIAQKNTPADVFIYFTDNETPAGVHPALALRE 485
 DB 447 SDMTLMQVAGLIIQTGGSTDCSLPITYASENEKTVDFIILTNQGT-GENEPMADILKM 505
 QY 486 YRKQNDIPAKLIVCGMTSNGFTIADPDDRGMLDMGCFPTGALDIVIRNFTLDM 537
 DB 506 YRKSSSVSKLVVCGLIANNLSIADPEDCGMLDTCGFSQAVDVHNFALDI 557
 RESULT 14
 Q5LJ97 HUMAN PRELIMINARY; PRT; 244 AA.
 Q5LJ97
 AC 05LJ97
 DT 01-FEB-2005 (TREMBlrel. 29, Created)
 DT 01-FEB-2005 (TREMBlrel. 29, Last sequence update)
 DT 01-FEB-2005 (TREMBlrel. 29, Last annotation update)
 DE Sjogren syndrome antigen A2 (60kDa, ribonucleoprotein autoantigen SS-

DE A/Ro) (Fragment).
 GN Name=SSA2; ORFNames=RP11-101E13.3-004;
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 ON NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Whitehead S.;
 RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL136370; CA110825.1; -, Genomic DNA.
 DR GO; GO:0030529; C:ribonucleoprotein complex; IEA.
 DR GO; GO:0003723; F:RNA binding; IEA.
 DR InterPro; IPR008858; TROVE.
 DR Pfam; PF05731; TROVE; 1.
 DR PROSITE; PS50988; TROVE; 1.
 KM Ribonucleoprotein; Viral nucleoprotein.
 FT NON TER
 SQ SEQUENCE 244 AA; 28035 MW; 92C174AF01E93B1 CRC64;
 Query Match 45.4%; Score 1265; DB 2; Length 244;
 Best Local Similarity 99.6%; Pred. No. 9e-77;
 Matches 243; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MESSVNMQPLNEKQJANSODGYVQVTDNNRLHRLFCFSGSEGGTYIKKQKGLNVAALIRLIE 60
 DB 1 MESSVNMQPLNEKQJANSODGYVQVTDNNRLHRLFCFSGSEGGTYIKKQKGLNVAALIRLIE 60
 QY 61 LIRLIEDGRCEVYIOEIKFSQSEGRITKQEPMLFALAICSCQSDISTKQAFKAVSEVCR 120
 DB 61 LIRLIEDGRCEVYIOEIKFSQSEGRITKQEPMLFALAICSCQSDISTKQAFKAVSEVCR 120
 QY 121 IPTHLPFIQPKDKESMKCGMGRALRKALADWYNEKGMALALAVTKYKQNGSHK 180
 DB 121 IPTHLPFIQPKDKESMKCGMGRALRKALADWYNEKGMALALAVTKYKQNGSHK 180
 QY 181 DILRLSHLKSSSEGLAVTKYITKGMKVEHLYEKALSVTEKLLKYLAWEKVKTKQLEVIYI 240
 DB 181 DILRLSHLKSSSEGLAVTKYITKGMKVEHLYEKALSVTEKLLKYLAWEKVKTKQLEVIYI 240
 QY 241 ELKV 244
 DB 241 ELKV 244
 RESULT 15
 O61K10 CABBR PRELIMINARY; PRT; 644 AA.
 AC O61K10
 DT 25-OCT-2004 (TREMBlrel. 28, Created)
 DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
 DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
 DE Hypothetical protein CBG09566.
 GN Name=CBG09566;
 OS Caenorhabditis briggsae.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditidae; Rhabditioidea;
 OC Rhabditidae; Peloderidae; Caenorhabditis.
 ON NCBI_TaxID=6238;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RG The C.briggsae Sequencing Consortium;
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 preliminary data.
 CC EMBL; CA001000044; CAB64775.1; -, Genomic DNA.
 DR GO; GO:0030529; C:ribonucleoprotein complex; IEA.
 DR GO; GO:0003723; F:RNA binding; IEA.
 DR InterPro; IPR008858; TROVE.
 DR Pfam; PF05731; TROVE; 1.
 DR PROSITE; PS50988; TROVE; 1.
 KM Hypothetical protein.

SEQ	SEQUENCE	644 AA; 72850 MW; AEB7EB0E0D7DEB5 CRC64;
Query Match	36.5%;	Score 1017.5; DB 2; Length 644;
Best Local Similarity	36.7%;	Pred. No. 1.3e-59;
Matches 216;	Conservative 108;	Mismatches 201; Indels 63; Gaps 8;
QY	7 QMGPINEKOTANGODGVVQVMDTNMRHLRPLCFSGSEGGTYIYKEOKLGLNENALIRLIE 66	
DB	54 QMEQVKEGQVNNAGGFVFPVSDETQYRRPLIGSDKGYTHQNAEKITLDNAQRIYIEIIQ 113	
QY	67 DGRGCEVIOEIKSPQSEGRITTKQEPMLFALICQSCSDISTKQ----- 109	
DB	114 KKGKHVYLHLELALINENRNPKNNSMLFTLACARVSTHDTTKNECPILHTYSEYIRAL 173	
QY	110 --AAPFAVSEVCRIPHTLFTFIOFKDKLKSMTKG-----MGRALRKALADYNKEGG 161	
DB	174 HAAALRLPLPVCRTPTLTFEFVYCCQTIASSTAGAKSSTGWGRSLRNALIKMYKEKTA 233	
QY	162 MALALAVTKYKORNGMSHKDLRLSHLKPSSBGL-----AIVTKYITKG----- 205	
DB	234 EKLAMLTITKTPQREGSHRDLFRLAHENLMDGTHTHTRDRLERBQLFRFAVKGDLVKA 293	
QY	206 -----MKVHELYKEKALSV-----ETEKLLKYLEAVEKVKRTKDELEVIHL 247	
DB	294 KKKANDEEKAKIEBSMDKRALKVYTEQQLVKEKSRALDLVEAYLSLKQEQSEVIYEA 353	
QY	248 IEBHRLVREHLTNHLKSKEVWKALLO-EMPLTALLNLGKMTANSVLEPGNSEVSLVCE 306	
DB	354 IKKGGLVREHLPTSSLSKLVMETLFDVPMPMTAMIRNLGKMTLVGALD--DNRVKSIVS 411	
QY	307 KLGNEKLLKKARLHPHILLALEYTKTGHLRGKLKWRPDEILKALDAAFYTKPTKVEP 366	
DB	412 RLTDQBELRRARLHPLTLTARSYVARGQDKSLTWEPNOKICDALLEAGFYKAFVNSPP 471	
QY	367 TGRKFLTAVDVSAWMQNVLSILNASTVAAAMCMVVTREKDSYVAFSDEWPCPVTT 426	
DB	472 TGRKYCALALVSGMSPVSSPLSCREAAATGMSLINLHNEABVCVAFCDKLTLPFTK 531	
QY	427 DMTLQOVLAMSGQIPAGCTCCSLPMIWAQKTNTPADVFIYFTDNETPAGVHPALALREY 486	
DB	532 DWKIGQVNDVNNLSFGSTDCGLPMTWATENNLLKFDVFIITYDNDTWAGEIHPEALIKKY 591	
QY	487 RKGMIDI-PAKLIVCGMTNSGFTIADPDDRGMLDWCGFDTGALDVIYRNF 533	
DB	592 REASGIDHAKVIVAMQAVNYISIDPSDAGMLDTGFDSAVPOIVHEF 639	

Search completed: January 13, 2006, 11:10:41
Job time : 78 secs